

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: November 14, 2006, 19:51:35 ; Search time 29.5576 Seconds
(without alignments)
4176.460 Million cell updates/sec

Title: US-10-619-359A-4

Perfect score: 6443

Sequence: 1 MDLEGRNGGAKEKFFKLN.....LAQGIYFPMVSVQAGAKRQ 1283

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 80.*
1: PIR.*
2: PIR.*
3: PIR.*
4: PIR.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6312.5	96.4	1280	1 DVHUI	multidrug resistan
2	5693	88.4	1276	1 DVHYIC	multidrug resistan
3	5677.5	88.1	1276	2 A34786	multidrug resistan
4	5303.5	82.3	1276	1 DVMS1	multidrug resistan
5	5230	81.2	1277	2 JH0502	p-glycoprotein - r
6	5032	78.1	1104	1 DVMS1A	multidrug resistan
7	4953	76.9	1279	1 DVHUS	multidrug resistan
8	4872.5	75.6	1276	1 DVMS2	multidrug resistan
9	4866	75.5	1281	2 T48123	p-glycoprotein iso
10	4838.5	75.1	1278	2 S41646	p-glycoprotein - r
11	4430.5	68.8	1287	2 S55692	multidrug resistan
12	3238.5	50.3	1321	2 T42228	p-glycoprotein sis
13	3234.5	50.2	1321	2 T42842	bile salt transpor
14	2892	44.9	1294	2 T19982	hypothetical prote
15	2846.5	44.2	1289	2 D87789	protein C3466.4 [i
16	2832.5	44.0	1275	2 T31073	multidrug resistan
17	2756.5	42.8	1321	2 T23476	hypothetical prote
18	2754.5	42.8	1321	2 T27337	multidrug resistan
19	2714.5	42.1	655	1 DVHY2C	multidrug resistan
20	2658	41.3	1283	2 A47377	multidrug resistan
21	2640	41.0	1286	2 T02187	probable ABC trans
22	2639.5	41.0	1292	2 T48007	p-glycoprotein hom
23	2602.5	40.4	1278	2 E86155	probable ABC trans
24	2574.5	40.0	1302	2 A41249	multidrug resistan
25	2543.5	39.5	1229	2 D85023	p-glycoprotein-lik
26	2540.5	39.4	1229	2 T52319	p-glycoprotein-lik
27	2531.5	39.3	1229	2 E85023	probable p-glycop
28	2511.5	39.0	1229	2 P86155	probable ABC trans
29	2482.5	38.5	1302	2 B41249	multidrug resistan

hypothetical prote
multidrug resistan
multidrug resistan
p-glycoprotein pgp
hypothetical prote
multidrug resistan
hypothetical prote
hypothetical prote
p-glycoprotein C -
hypothetical prote
p-glycoprotein 2 -
multidrug resistan
multidrug resistan
leptomycin B resis
hypothetical prote
hypothetical prote
probable p-glycop

ALIGNMENTS

RESULT 1

DVHUI

multidrug resistance protein 1 - human

N; Alternate names: P-glycoprotein 1

C; Species: Homo sapiens (man)

C; Date: 31-Dec-1990 #sequence revision 18-Aug-1995 #text change 09-Jul-2004

C; Accession: A34914; PS0162; S15500; A25059; S43838; I52238; I65204

X; Chen, C.; Clark, D.; Ueda, K.; Pastan, I.; Gottesman, M.M.; Roninson, I.B.

J. Biol. Chem. 265, 506-514, 1990

A; Title: Genomic organization of the human multidrug resistance (MDR1) gene and origin

A; Reference number: A34914; MUID:90094448; PMID:1967175

A; Accession: A34914

A; Molecule type: DNA

A; Residues: 1-1280 <CH>

A; Cross-references: UNIPROT:P08183; UNIPARC:UPI000003BD16; GB:M29447; GB:J05168; NID:G1

R; Kioka, N.; Yamano, Y.; Romano, T.; Ueda, K.

submitted to JIPID, April 1991

A; Reference number: PS0162

A; Accession: PS0162

A; Molecule type: DNA

A; Residues: 1-22 <KIO>

A; Cross-references: UNIPARC:UPI00001746C8

R; Kioka, N.; Yamano, Y.; Romano, T.; Ueda, K.

submitted to the EMBL Data Library, April 1991

A; Description: Transcriptional regulation of multidrug resistance gene (MDR1) expression

A; Reference number: S15500

A; Accession: S15500

A; Molecule type: DNA

A; Residues: 1-22, 'R' <KI2>

A; Cross-references: UNIPARC:UPI000016AD22; EMBL:X58723; NID:G34522; PIDN:CAA41558.1; PI

R; Chen, C.; Chin, J.E.; Ueda, K.; Clark, D.P.; Pastan, I.; Gottesman, M.M.; Roninson, I

Cell 47, 381-389, 1986

A; Title: Internal duplication and homology with bacterial transport proteins in the mdr

A; Reference number: A25059; MUID:87028230; PMID:2876781

A; Accession: A25059

A; Molecule type: mRNA

A; Residues: 1-184, 'V', 186-1280 <CH2>

A; Cross-references: UNIPARC:UPI0000039699; GB:M14758; NID:G187468; PIDN:AAA59575.1; PID

R; Chambers, T.C.; Pohl, J.; Glads, D.B.; Kuo, J.F.

Biochem. J. 299, 303-315, 1994

A; Title: Phosphorylation by protein kinase C and cyclic AMP-dependent protein kinase of

A; Reference number: S43838; MUID:94220047; PMID:7909431

A; Accession: S43838

A; Molecule type: protein

A; Residues: 656-689 <CHA>

A; Cross-references: UNIPARC:UPI00001746C9

R; Gekeler, V.; Weger, S.; Probst, H.

Biochem. Biophys. Res. Commun. 169, 796-802, 1990

A; Title: mdr1/P-glycoprotein gene segments analyzed from various human leukemic cell li

A; Reference number: I52238; MUID:90290529; PMID:1972623

A; Accession: I52238

A; Status: translated from GB/EMBL/DBJ

A;Molecule type: DNA
 A;Residues: 178-215 <RES>
 A;Cross-references: UNIPARC:UPI000016A03C; GB:M37724; NID:g183537; PIDN:AAA88047.1; PID:
 A;Accession: 155204
 A;Status: translated from GB/EMBL/DBD
 A;Molecule type: DNA
 A;Residues: 800-856 <RE2>
 A;Cross-references: UNIPARC:UPI000016A03D; GB:M37725; NID:g183538; PIDN:AAA88048.1; PID:
 C;Comment: This is an integral membrane protein overproduced in multidrug-resistant cell
 structurally and functionally unrelated lipophilic anticancer drugs.
 C;Genetics:
 A;Gene: GDB:PGV1; MDR1
 A;Cross-references: GDB:120712; OMIM:171050
 A;Map position: 7q21-7q21
 C;Superfamily: multidrug resistance protein; ATP-binding cassette homology
 C;Keywords: ATP; duplication; glycoprotein; nucleotide binding; P-loop; phosphoprotein;
 P1:638,653-1280/Region: duplication
 P1:638,653-1280/Region: duplication
 F1:49-350/Domain: hydrophobic <HB1>
 F1:351-637/Domain: hydrophobic <HB1>
 F1:427-434/Region: nucleotide-binding motif A (P-loop)
 F1:551-555/Region: nucleotide-binding motif B
 F1:638-708/Domain: linker <LIN>
 F1:709-993/Domain: hydrophobic <HB2>
 F1:994-1280/Domain: hydrophobic <HB2>
 F1:1053-1249/Domain: ATP-binding cassette homology <ABC2>
 F1:1070-1077/Region: nucleotide-binding motif A (P-loop)
 F1:1196-1200/Region: nucleotide-binding motif B
 F1:91.94.99/Binding site: carboxylate (Asn) (covalent) #status predicted
 F1:433/Binding site: ATP (Lys) #status predicted
 F1:661,667/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status exp
 F1:667,671/Binding site: phosphate (Ser) (covalent) (by CAMP-dependent kinase) #statu
 F1:1076/Binding site: ATP (Lys) #status predicted

Query Match 96.4%; Score 6212.5; DB 1; Length 1280;
 Best Local Similarity 96.5%; Pred. No. 0;
 Matches 1236; Conservativs 18; Mismatches 24; Indels 3; Gaps 1;

Qy 1 MDLEGRNGGAKKQKFFLNKSKDCKKERTPTVSFVSFMYSNWLDKLYMVVGTAAII 60
 Db 1 MDLEGRNGGAKKQKFFLNKSKDCKKERTPTVSFVSFMYSNWLDKLYMVVGTAAII 60
 Qy 61 HGAGLPLMLVFGDMTTFANAGNLGDLGALLFANTSSNITDTVPWNLEEDMTRVAY 120
 Db 61 HGAGLPLMLVFGDMTTFANAGNLGDLGALLFANTSSNITDTVPWNLEEDMTRVAY 120
 Qy 61 HGAGLPLMLVFGDMTTFANAGNLGDLGALLFANTSSNITDTVPWNLEEDMTRVAY 117
 Db 61 HGAGLPLMLVFGDMTTFANAGNLGDLGALLFANTSSNITDTVPWNLEEDMTRVAY 117
 Qy 121 YSGIGAGVLAAYIQVSWFCLAGQIHKIRKQFPHAIMRQEIQWDFVHDVDELNTRLTD 180
 Db 121 YSGIGAGVLAAYIQVSWFCLAGQIHKIRKQFPHAIMRQEIQWDFVHDVDELNTRLTD 177
 Qy 181 DVSKINEGIDKIGMPTQSNATPTFTGIVGTRGWLTLVLAIQWGLSAVVAWAKILS 240
 Db 181 DVSKINEGIDKIGMPTQSNATPTFTGIVGTRGWLTLVLAIQWGLSAVVAWAKILS 237
 Qy 241 SPTDKELLAYAKAGAEVLAARTVTAFGGQKKELERYNNKLEAKRIGIKKAITANI 300
 Db 238 SPTDKELLAYAKAGAEVLAARTVTAFGGQKKELERYNNKLEAKRIGIKKAITANI 297
 Qy 301 SIGAFLIIYASALAFWYGTTLVLSKEYSIGQVTLVPSFVLIQAFSGVQASPSIEAFAN 360
 Db 298 SIGAFLIIYASALAFWYGTTLVLSKEYSIGQVTLVPSFVLIQAFSGVQASPSIEAFAN 357
 Qy 361 ARGAAFIKIIDNKPISDSYSGKHPDNTKGNLFNPNVPSPSRKEVKILGMLKV 420
 Db 358 ARGAAFIKIIDNKPISDSYSGKHPDNTKGNLFNPNVPSPSRKEVKILGMLKV 417
 Qy 421 QSGOTVALVNSGCGKSTTVQMLORLYDPTSGMVSVDQDRTINVRFLRIIGVSOEP 480
 Db 418 QSGOTVALVNSGCGKSTTVQMLORLYDPTSGMVSVDQDRTINVRFLRIIGVSOEP 477
 Qy 481 VLPATTIAENIRYGRVDVTDIEKAVKBNAYDFIMKLPOKFDTLVGERGAQLSGGQK 540
 Db 478 VLPATTIAENIRYGRVDVTDIEKAVKBNAYDFIMKLPOKFDTLVGERGAQLSGGQK 537

Qy 541 RTAARALVRNPKILLDLBATSALDTESEAVVQVALDKARKGRTTIVIAHRLSTVRNADY 600
 Db 538 RTAARALVRNPKILLDLBATSALDTESEAVVQVALDKARKGRTTIVIAHRLSTVRNADY 597
 Qy 601 IAGPDDGVIVEKGNHDELAKKGIYFKLVTMTAGNEIELENAADESKSEIDTLEMSHD 660
 Db 598 IAGPDDGVIVEKGNHDELAKKGIYFKLVTMTAGNEIELENAADESKSEIDTLEMSHD 657
 Qy 661 SSSSLIRKSTERSVRGSGQDQKLSKALDESIPPSVFWIMKLNLTWEPYFVVGVC 720
 Db 658 SSSSLIRKSTERSVRGSGQDQKLSKALDESIPPSVFWIMKLNLTWEPYFVVGVC 717
 Qy 721 AIINGLOPAPAVIFSIIIGITFRNDDBATKQNSLPSLLFLVLGIVSFIFFLOGFTF 780
 Db 718 AIINGLOPAPAVIFSIIIGITFRNDDBATKQNSLPSLLFLVLGIVSFIFFLOGFTF 777
 Qy 781 GKAGEILTTLRLRYMFRSMRLRODVSWFDDPKNTTGAITTLRLANDAAQVKGALGSLRAIT 840
 Db 778 GKAGEILTTLRLRYMFRSMRLRODVSWFDDPKNTTGAITTLRLANDAAQVKGALGSLRAIT 837
 Qy 841 QNTANLGTGIIISLIYGMOLTLLALLAIVPIIAIAGVVMKMLSGQALKDKKLEAGAKIA 900
 Db 838 QNTANLGTGIIISLIYGMOLTLLALLAIVPIIAIAGVVMKMLSGQALKDKKLEAGAKIA 897
 Qy 901 TEAIENFRVTSLSLTQOKFHEMYDQSLQVYNSLRKAHIFGITESTQAMMYFSYAGCF 960
 Db 898 TEAIENFRVTSLSLTQOKFHEMYDQSLQVYNSLRKAHIFGITESTQAMMYFSYAGCF 957
 Qy 961 RFCAVLVAHSLMSFEDVLVFAVFGMAVQVSSFADYAKAKYSAAHIMIEKTP 1020
 Db 958 RFCAVLVAHSLMSFEDVLVFAVFGMAVQVSSFADYAKAKYSAAHIMIEKTP 1017
 Qy 1021 IDSYSTGLKPNTEGNTFNVFNYPRLDIPVLQGLSLEVKKQOTLALVSSSCGGS 1080
 Db 1018 IDSYSTGLKPNTEGNTFNVFNYPRLDIPVLQGLSLEVKKQOTLALVSSSCGGS 1077
 Qy 1081 TVVOLLERFVPLAGKVLDDGKEIKOLNVQWLAHGIQVSRPILPDCGISENIAYGDNS 1140
 Db 1078 TVVOLLERFVPLAGKVLDDGKEIKOLNVQWLAHGIQVSRPILPDCGISENIAYGDNS 1137
 Qy 1141 RVVSQSEIVRAAKEANIHAIESLPNKYSTKVDGKTQSGQKQRIARALVRPHIL 1200
 Db 1138 RVVSQSEIVRAAKEANIHAIESLPNKYSTKVDGKTQSGQKQRIARALVRPHIL 1197
 Qy 1201 LDEATSAIDTSEKVVQBALDKAREGRTCVIAHRLSTIONADLVFQNGRVEHGH 1260
 Db 1198 LDEATSAIDTSEKVVQBALDKAREGRTCVIAHRLSTIONADLVFQNGRVEHGH 1257
 Qy 1261 QQLAOKGIVFSMVSVQAGAKQ 1283
 Db 1258 QQLAOKGIVFSMVSVQAGAKQ 1280

RESULT 2

DMVLC

multidrug resistance protein 1 - Chinese hamster

N;Alternate names: P-glycoprotein pgp1

C;Species: Cricetus griseus (Chinese hamster)

C;Date: 31-Dec-1990 #sequence revision 30-Sep-1992 #text change 09-Jul-2004

C;Accession: A38696; B38696; A27126; S33768; I52823

R;Devine, S.B., Huggain, A.; Davide, J.P.; Melera, P.W.

J. Biol. Chem. 266, 4545-4555, 1991

A;Title: Full length and alternatively spliced pgp-1 transcripts in multidrug-resistant

A;Reference number: A38696; MUID:91154265; PMID:1671863

A;Accession: A38696

A;Molecule type: mRNA

A;Residues: 1-1276 <DEV>

A;Cross-references: UNIPROT:P21448; UNIPARC:UPI000004FE21; GB:M59253; NID:g191154; PIDN

A;Accession: C38696

A;Molecule type: mRNA

A;Residues: 108-1276

A;Cross-references: UNIPARC:UPI000008642; GB:M59254; NID:g191156; PIDN:AAA37005.1; PID

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OM protein - protein search, using sw model

Run on: November 14, 2006, 19:51:35 ; Search time 29.5576 Seconds
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Title: US-10-619-359A-4
Perfect score: 6443
Sequence: 1 MDLEGRNGAEKKNFFKLN.....LAQGIYFMSVQAGAKSQ 1283

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Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80: *
1: p1r1: *
2: p1r2: *
3: p1r3: *
4: p1r4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	6212.5	96.4	1280	1 DVH01	multidrug resist
2	5693	88.4	1276	1 DVH1C	multidrug resist
3	5677.5	88.1	1276	2 A34786	multidrug resist
4	5303.5	82.3	1276	1 DVMS1	multidrug resist
5	5230	81.2	1277	2 DVH0502	p-glycoprotein - r
6	5032	78.1	1104	1 DVMS1A	multidrug resist
7	4953	76.9	1279	1 DVH03	multidrug resist
8	4872.5	75.6	1276	1 DVMS2	multidrug resist
9	4866	75.5	1281	2 I48123	p-glycoprotein iso
10	4838.5	75.1	1278	2 I48146	p-glycoprotein - r
11	4430.5	68.8	1287	2 S55692	multidrug resist
12	4238.5	50.3	1321	2 T42228	p-glycoprotein sis
13	3234.5	50.2	1321	2 T42842	bile salt transpor
14	2892	44.9	1294	2 T19882	hypothetical prote
15	2846.5	44.2	1289	2 D87789	protein C3466.4 [i
16	2832.5	44.0	1275	2 T31073	multidrug resist
17	2756.5	42.8	1321	2 T23476	hypothetical prote
18	2754.5	42.8	1321	2 S27337	multidrug resist
19	2714.5	42.1	655	1 DVH2C	multidrug resist
20	2658	41.3	1283	2 A47377	multidrug resist
21	2640	41.0	1286	2 T02187	probable ABC trans
22	2639.5	41.0	1292	2 T48007	P-glycoprotein hom
23	2602.5	40.4	1278	2 E86155	probable ABC trans
24	2574.5	40.0	1302	2 A41249	multidrug resist
25	2543.5	39.5	1229	2 D85023	P-glycoprotein-lik
26	2540.5	39.4	1229	2 T52319	P-glycoprotein-lik
27	2531.5	39.3	1230	2 E85023	probable P-glycop
28	2511.5	39.0	1229	2 F86155	probable ABC trans
29	2482.5	38.5	1302	2 B41249	multidrug resist

30	2467	38.3	1323	2 H85202	hypothetical prote
31	2447	38.0	1408	2 T43261	multidrug resist
32	2419.5	37.6	1310	2 S30328	multidrug resist
33	2417.5	37.5	1286	2 A42150	P-glycoprotein ppp
34	2416	37.5	1268	2 T22094	hypothetical prote
35	2413.5	37.5	1302	2 S30327	multidrug resist
36	2412	37.4	1266	2 T22090	hypothetical prote
37	2363	36.7	1254	2 S27338	P-glycoprotein C -
38	2361	36.6	1222	2 T14805	hypothetical prote
39	2314.5	35.9	1233	2 T04251	P-glycoprotein 2 -
40	2300	35.7	1254	2 T30855	multidrug resist
41	2290.5	35.6	1307	2 T30882	multidrug resist
42	2279.5	35.4	1362	2 T41534	leptomycin B resis
43	2273	35.3	1318	2 T21266	hypothetical prote
44	2238.5	34.7	1327	2 T21268	hypothetical prote
45	2228	34.6	1245	2 G86404	probable P-glycop

ALIGNMENTS

RESULT 1
DVH01
Multidrug resistance protein 1 - human
N:Alternate names: P-glycoprotein 1
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1990 #sequence revision 18-Aug-1995 #text change 09-Jul-2004
C:Accession: A34914; PS0162; S15500; A25059; S43838; I52238; I52238; I52238
R:Chen, C.; Clark, D.; Ueda, K.; Pastan, I.; Gottesman, M.M.; Roninson, I.B.
J. Biol. Chem. 265, 506-514, 1990
A:Title: Genomic organization of the human multidrug resistance (MDR1) gene and origin
A:Reference number: A34914; MUID:90094448; PMID:1967175
A:Accession: A34914
A:Molecule type: DNA
A:Residues: 1-1280 <CHE>
R:Kioaka, N.; Yamano, Y.; Komano, T.; Ueda, K.
submitted to JIPID, April 1991
A:Reference number: PS0162
A:Accession: PS0162
A:Molecule type: DNA
A:Residues: 1-22 <KIO>
A:Cross-references: UNIPROT:P08183; UNIPARC:UPI000003BD16; GB:M29447; GB:J05168; NID:gl
R:Kioaka, N.; Yamano, Y.; Komano, T.; Ueda, K.
submitted to the EMBL Data Library, April 1991
A:Description: Transcriptional regulation of multidrug resistance gene (MDR1) expressio
A:Reference number: S15500
A:Accession: S15500
A:Molecule type: DNA
A:Residues: 1-22, 'R' <K12>
A:Cross-references: UNIPARC:UPI000016AD22; EMBL:X58723; NID:G34522; PIDN:CAA41558.1; PI
R:Chen, C.; Chin, J.E.; Ueda, K.; Clark, D.P.; Pastan, I.; Gottesman, M.M.; Roninson, I
Cell 47, 381-389, 1986
A:Title: Internal duplication and homology with bacterial transport proteins in the mdr
A:Reference number: A25059; MUID:87028230; PMID:2876781
A:Accession: A25059
A:Molecule type: mRNA
A:Residues: 1-184, 'V', 186-1280 <CH2>
A:Cross-references: UNIPARC:UPI0000039699; GB:M14758; NID:gl87468; PIDN:AAA59575.1; PID
R:Chambers, T.C.; Pohl, J.; Glass, D.B.; Kuo, J.F.
Biochem. J. 299, 309-315, 1994
A:Title: Phosphorylation by protein kinase C and cyclic AMP-dependent protein kinase of
A:Reference number: S43838; MUID:94220047; PMID:7909431
A:Accession: S43838
A:Molecule type: protein
A:Residues: 656-689 <CHA>
A:Cross-references: UNIPARC:UPI00001746C9
R:Geleler, V.; Weger, S.; Probst, H.
Biochem. Biophys. Res. Commun. 169, 796-802, 1990
A:Title: mdr1/P-glycoprotein gene segments analyzed from various human leukemic cell li
A:Reference number: I52238; MUID:90290529; PMID:1972623
A:Accession: I52238
A>Status: translated from GB/EMBL/DBJ

RESULT 2
DVHYLC

A;Experimental source: clone ADX185
 A;Accession: B38696
 A;Molecule type: mRNA
 A;Residues: 1-32,771-1276 <DE2>
 A;Cross-references: UNIPARC:UPI000000E6F3F; GB:M59252; NID:g191152; PIDN:AAA37003.1; PID:
 R;Endicott, J.A.; Juranaka, P.F.; Sarangi, F.; Gerlach, J.H.; Deuchars, K.L.; Ling, V.
 Mol. Cell. Biol. 7, 4075-4081, 1987
 A;Title: Simultaneous expression of two P-glycoprotein genes in drug-sensitive Chinese h
 A;Reference number: A27126
 A;Accession: A27126
 A;Status: not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 706-1276 <END>
 A;Cross-references: UNIPARC:UPI0000170730; GB:M17897; NID:g191159; PIDN:AAA37006.1; PID:
 R;Zastawny, R.L.; Ling, V.
 Biochim. Biophys. Acta 1173, 303-313, 1993
 A;Title: Structural and functional analysis of 5' flanking and intron 1 sequences of the
 A;Reference number: S33768; MUID:93305724; PMID:8100449
 A;Accession: S33768
 A;Status: translation not shown
 A;Molecule type: DNA
 A;Residues: 1-21 <ZAS>
 A;Cross-references: UNIPARC:UPI00001746CA; EMBL:L03286
 R;Teeter, L.D.; Eckersberg, T.; Tsai, Y.; Kuo, M.T.
 Cell Growth Differ. 2, 429-437, 1991
 A;Title: Analysis of the Chinese hamster P-glycoprotein/multidrug resistance gene pgp1
 A;Reference number: 152823; MUID:92089970; PMID:1661134
 A;Accession: 152823
 A;Status: translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-21 <RES>
 A;Cross-references: UNIPARC:UPI00001746CA; GB:881975; NID:g240862
 C;Comment: This is an integral membrane protein overproduced in multidrug-resistant cell
 structurally and functionally unrelated lipophilic antitumor drugs.
 C;Genetics:
 A;Gene: pgp1
 C;Superfamily: multidrug resistance protein; ATP-binding cassette homology
 C;Keywords: alternative splicing; ATP; duplication; glycoprotein; nucleotide binding; P-
 F:407-601/Domain: ATP-binding cassette homology <ABC1>
 F:424-431/Region: nucleotide-binding motif A (P-loop)
 F:548-552/Region: nucleotide-binding motif B
 F:1050-1246/Domain: ATP-binding cassette homology <ABC2>
 F:1067-1074/Region: nucleotide-binding motif A (P-loop)
 F:1193-1197/Region: nucleotide-binding motif B
 F:87,91,96/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:430/Binding site: ATP (Lys) #status predicted
 F:1073/Binding site: ATP (Lys) #status predicted

Query Match 88.4%; Score 5693; DB 1; Length 1276;
 Best Local Similarity 86.7%; Pred. No. 1.7e-312;
 Matches 1112; Conservative 89; Mismatches 75; Indels 6; Gaps 3;
 QY 1 MDLEGRNGAGKKNFKLNKSKDKKCKPVSVPSPRYSNMLDKLVMVGTAAII 60
 DB 1 MFEEDFS-GRKDNFLKGRKSKKCKKPPVSVFTMFYAGWLDRLVLMVGTAAII 59
 QY 61 HGAGLPMLVFGDMTDTFANAGNLGDLGALLFNNTNNSNITDTPVMNLEEDTRYAY 120
 DB 60 HGVALPMLVFGDMTDSFASVGNIPFNAT--NNATQVNASDI FG--KLEEMTYAY 114
 QY 121 YSGIGAGLVAAIYQVSWFCLAAAGROHKIRKQFPHAIMRQEI GWFDFVHDVGLNTRLTD 180
 DB 115 YTGIGAGLVAAIYQVSWFCLAAAGROHKIRKQFPHAIMRQEI GWFDFVHDVGLNTRLTD 174
 QY 181 DYSKINEGIDGKIMFQSNATPFTTGIVGTGKLTVLTAISPVGLSAAVAKILS 240
 DB 175 DYSKINEGIDGKIMFQSNATPFTTGIVGTGKLTVLTAISPVGLSAAVAKILS 234
 QY 241 SPTDKELAYAKAGAAVEEVLAAIRTVIAFGGQKGLERYNKNLEBAKIGIKKAITANI 300
 DB 235 SPTDKELAYAKAGAAVEEVLAAIRTVIAFGGQKGLERYNKNLEBAKIGIKKAITANI 294

RESULT 3

A34786

multidrug resistance protein 1a - mouse
 C:Species: Mus musculus (house mouse)

QY 301 SIGNAFLLIYASALAPFWYGTTLVLKEYSIGQVLTVPFFSVLIGAPVGQASPEIEAFAN 360
 DB 295 SMGAFFLLIYASALAPFWYGTSLVLSKEYSIGQVLTVPFFFAVLIAFPFSGOASPNIEAFAN 354
 QY 361 ARGAAPEIFKIIDNKPSIDSYSGHGKPDNI KGNLEPRNVHFSYPSRKEVKILKGLNLKV 420
 DB 355 ARGAAPEIFNIIDNKPSIDSFSGNGYKPDNI KGNLEFNIHFSYPSRKYVILKGLNLKV 414
 QY 421 QSGOTVALVGNSCGKSTTVQLMORLYDPTTEGMVSDGDQIRTNVRLREIIGVVSQEP 480
 DB 415 QSGOTVALVGNSCGKSTTVQLMORLYDPTTEGMVSDGDQIRTNVRLREIIGVVSQEP 474
 QY 481 VLPATTIAENIRYGRDVTWDETEKAVKEANAYDFIMKLPQKFDTLVGERGAOLSGQKQ 540
 DB 475 VLPATTIAENIRYGRDVTWDETEKAVKEANAYDFIMKLPKFDTLVGERGAOLSGQKQ 534
 QY 541 RIAAALVRNPKILLDEATSAIDTESEAVVOVALDKARKGRTTIVIAHRLSTVRNADV 600
 DB 535 RIAAALVRNPKILLDEATSAIDTESEAVVOVALDKARKGRTTIVIAHRLSTVRNADI 594
 QY 601 IAGFDGVIIVEKGNHDELMKEGIYFKLVMTQAGNEIELENAADBSKSIDTLEMSSHD 660
 DB 595 IAGFDGVIIVEKGNHDELMKEGIYFKLVMTQAGNEIELENEVSGSKNEIDNLDMSKD 654
 QY 661 SSSLLIRKSTRSVRGSGODRKLTKEALDESIPVPSFWIRIMKLNLTWPFYVGVPC 720
 DB 655 SASSLLIRSTRSIRSGPHDQDKLTKEALDEDPVPSFWIRILKLNLSWPFYVGVPC 714
 QY 721 AIINGLOPAPAVIPSKIGITPTNDDAETKQNSLFSLLFLVLGIVSPTIFLOGFTF 780
 DB 715 AIYNGALQPAFSIIFSKVGVFTNDDDETKRHSNLSLFLVLGIVSPTIFLOGFTF 774
 QY 781 GKAGEILTRLRYMFRSMLRDQVSWFDDPKNTTGALTTLRLANDAAQVKAIGASRLAIT 840
 DB 775 GKAGEILTRLRYMFRSMLRDQVSWFDDPKNTTGALTTLRLANDAAQVKGATGARLAVIT 834
 QY 841 QNIANLGTGIIISLIYGMQTLTLLAIVPIIAIAGVEMKMLSGQALKDKKKELEGSKIA 900
 DB 835 QNIANLGTGIIISLIYGMQTLTLLAIVPIIAIAGVEMKMLSGQALKDKKKELEGSKIA 894
 QY 901 TEAIENFRTVSLTQKPEHMYDOSLOVPYNSLRKAHIFGTFESFTQAMMYFSYAGCF 960
 DB 895 TEAIENFRTVSLTQKPEHMYDOSLOVPYNSLRKAHIFGTFESFTQAMMYFSYAGCF 954
 QY 961 RFGAVILVAHSLMSFEDVLVFSAVVFGAMAVGVSSFPADYAKAKVSAAHIIIEKTP 1020
 DB 955 RFGAVILVAHSLMSFEDVLVFSAVVFGAMAVGVSSFPADYAKAKVSAAHIIIEKTP 1014
 QY 1021 IDSYSTGLKPNLTBGNVTTFNBNVFNYPTRLDIPVLQGLSLEVKKGTLLALVSSCGGKS 1080
 DB 1015 IDSYSTGLKPNLTBGNVTTFNBNVFNYPTRLDIPVLQGLSLEVKKGTLLALVSSCGGKS 1074
 QY 1081 TVVQLLERFYDPLAGKVLIDGKEIKQANVOMLAHLGTVSOPILFDCSISENIAYGDS 1140
 DB 1075 TVVQLLERFYDPMAGTVFLDGKEVQNLVQVLAHLGTVSOPILFDCSISENIAYGDS 1134
 QY 1141 RVVSQEEIVRAAKEANIHAFIESLPNKYSTRYVDGKTQLSGGQKORIAIARALVRQPHIL 1200
 DB 1135 RVVSQEEIVRAAKEANIHAFIESLPNKYSTRYVDGKTQLSGGQKORIAIARALVRQPHIL 1194
 QY 1201 LDEATSAIDTESEKVOEALDKAREGRTCVIAHRLSTIQNALDILVFPQGRVKEHGH 1260
 DB 1195 LDEATSAIDTESEKVOEALDKAREGRTCVIAHRLSTIQNALDILVFPQGRVKEHGH 1254
 QY 1261 QQLLAKGIYFSMVSVOAGAKR 1282
 DB 1255 QQLLAKGIYFSMVSVOAGAKR 1276

C>Date: 13-Jul-1990 #sequence_revision 13-Jul-1990 #text_change 09-Jul-2004
C/Accession: A34786; A35671
R/Devault, A.; Gros, P.
Mol. Cell. Biol. 10, 1652-1663, 1990
A/Title: Two members of the mouse mdr gene family confer multidrug resistance with overl
A/Reference number: A34786; MUID:90205845; PMID:1969610
A/Accession: A34786
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-1276 <DEV>
A/Cross-references: UNIPROT:P21447; UNIPARC:UPI0000028C58; GB:M30697; NID:G199111; PIDN:
R/Hsu, S.I.H.; Cohen, D.; Kirschner, L.S.; Lothstein, L.; Hartstein, M.; Horwitz, S.B.
Mol. Cell. Biol. 10, 3596-3606, 1990
A/Title: Structural analysis of the mouse mdr1a (P-glycoprotein) promoter reveals the ba
A/Reference number: A35671; MUID:90287150; PMID:1972547
A/Accession: A35671
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-525, 'HV', 528-938, 'S', 940-1035, 'V', 1037-1276 <HSU>
A/Cross-references: UNIPARC:UPI0000046660; GB:M33591; NID:G199104; PIDN:AAA39514.1; PID:
C/Suprafamily: multidrug resistance protein; ATP-binding cassette homology
C/Keywords: ATP; duplication; glycoprotein; membrane protein; nucleotide binding; P-loop
F:406-600/Domain: ATP-binding cassette homology <ABC1>
F:423-431/Region: nucleotide-binding motif A (P-loop)
F:547-551/Region: nucleotide-binding motif B
F:1049-1245/Domain: ATP-binding cassette homology <ABC2>
F:1066-1074/Region: nucleotide-binding motif A (P-loop)
F:1192-1196/Region: nucleotide-binding motif B
F:429/Binding site: ATP (lys) #status predicted
F:1072/Binding site: ATP (lys) #status predicted

Query Match 88.1%; Score 5677.5; DB 2; Length 1276;
Best Local Similarity 87.1%; Pred. No. 1.2e-311;
Matches 1116; Conservative 78; Mismatches 31; Indels 7; Gaps 2;

QY 1 MDLEGRNGAEKKNFFKLNKSKKDKKPKTVSVFSPRYSNWLDKLVVVGTLAAII 60
DB 1 MELEEDLKGRAD-KNFSKMGKSKKKEKPAVSLVTFRYAGWLDRLVNLVGTLLAAII 59
QY 61 HGAGLPLAMLVFGDMTDTTANAGNLGDLGALLFNNTSSNITPTVPVNLLEEDMTYAYY 120
DB 60 HGVALPLAMLVFGDMTDSFASVGNVSK-----NSTNMSEADKRAFKEEBMTYAYY 113
QY 121 YSGIGAGLVAAVIOVSFVCLAGROTHKIKQPFHAIKROEIGFVDVHDVGLNRLTD 180
DB 114 YTGIGAGLVIAVIOVSFVCLAGROTHKIKQPFHAIKROEIGFVDVHDVGLNRLTD 173
QY 181 DYSKINEGIDKIGMFFQSMATPFTGIVGFTGKWLTVILAIISPVLGLSAAVWAKILS 240
DB 174 DYSKINEGIDKIGMFFQSMATPFTGIVGFTGKWLTVILAIISPVLGLSAAVWAKILS 233
QY 241 SPTDKELAYAKAGAAVEVLAARTVIAFGGQKELRYNKNLEBAKIGIKKAITANI 300
DB 234 SPTDKELHAYAKAGAAVEVLAARTVIAFGGQKELRYNKNLEBAKIGIKKAITANI 293
QY 301 SIGAPELLIYASVALAFWTGTLVLKESVIGOVLFVFFSVLIGASVGOAPSIFAPAN 360
DB 294 SNGRAPELLIYASVALAFWTGTLVLKESVIGOVLFVFFSVLIGASVGOAPSIFAPAN 353
QY 361 ARGAAFEIKIINDKPSIDYSKSGHKPNKGNLEFRNVHFSYPSRKEVILKGLNKKV 420
DB 354 ARGAAFEIKIINDKPSIDYSKSGHKPNKGNLEFRNVHFSYPSRKEVILKGLNKKV 413
QY 421 QSGQTVLVGNSGCGKSTTVQLMORLYDPTGMSVSDGQDIRTINVRFLREIIGVVSQBP 480
DB 414 KSGQTVLVGNSGCGKSTTVQLMORLYDPLDGNVSDGQDIRTINVRFLREIIGVVSQBP 473
QY 481 VLPATTIAENIRYGRDVTMDIEKAVKANAYDFIMKLPQKPDVLVGRGQAGLGGQKQ 540
DB 474 VLPATTIAENIRYGRDVTMDIEKAVKANAYDFIMKLPQKPDVLVGRGQAGLGGQKQ 533
QY 541 RTAIRALVRNPKILLDLDEATSDALDTESEAVVQVVALDKARGRTTIVIAHRLSTVRNADV 600

534 RTAIRALVRNPKILLDLDEATSDALDTESEAVVQVVALDKARGRTTIVIAHRLSTVRNADV 593
QY 601 IAGFDDGVIVEKGNHDELMKEKGIYFKLVMTQTAGNEIELENAADESKSEIDTLESSH 660
DB 594 IAGFDDGVIVEKGNHDELMKEKGIYFKLVMTQTAGNEIELENADESKSEIDTLESSH 653
QY 661 SGSSLIIRKSTRSRVSGSQDQRKLTKEALDESIPVPSFWIMKLNLTENFYFVGVGFC 720
DB 654 SGSSLIIRKSTRSRVSGSQDQRKLTKEALDESIPVPSFWIMKLNLTENFYFVGVGFC 713
QY 721 AIINGLOPAPAVIFSKIGITRNDADFTKQNSLNLSLLFLVLGIVGIFITFFLQGGTF 780
DB 714 AIINGLOPAPAVIFSKIGITRNDADFTKQNSLNLSLLFLVLGIVGIFITFFLQGGTF 773
QY 781 GKAGBILTKRLRYMFRSMRLQDVSWFDDPKNTTGALTTRLANDAAQVKAIGSLAII 840
DB 774 GKAGBILTKRLRYMFRSMRLQDVSWFDDPKNTTGALTTRLANDAAQVKAIGSLAII 833
QY 841 QNANLGTGIIISLYGQTLTLLAIPIAIAGVEMKMLSGQALKDKKLEBAGKIA 900
DB 834 QNANLGTGIIISLYGQTLTLLAIPIAIAGVEMKMLSGQALKDKKLEBAGKIA 893
QY 901 TEAIENFRVSLTQEQKFEHMYDOSLOVPYRNSLRKAHIFGITFSFTQAMVYFVAGCF 960
DB 894 TEAIENFRVSLTQEQKFEHMYDOSLOVPYRNSLRKAHIFGITFSFTQAMVYFVAGCF 953
QY 961 RFGAYLVASHLMSFEDVLLVFSVAVFGAMVGVQSSFPADYAKAKVSAHIIIEKTP 1020
DB 954 RFGAYLVASHLMSFEDVLLVFSVAVFGAMVGVQSSFPADYAKAKVSAHIIIEKTP 1013
QY 1021 IDSYSTEGKNTLEGNTFNEVNYTRLDIPVLQGLSLEVKGQTLALVSSGCGKS 1080
DB 1014 IDSYSTEGKNTLEGNTFNEVNYTRLDIPVLQGLSLEVKGQTLALVSSGCGKS 1073
QY 1081 TVQQLLEFYDPLAGKVLDDGKEIKQLNVQWLRHGLIVTSQBPILFDCSISENIAVGDNS 1140
DB 1074 TVQQLLEFYDPLAGKVLDDGKEIKQLNVQWLRHGLIVTSQBPILFDCSISENIAVGDNS 1133
QY 1141 RVVSQEEIVRAAKEANIHAFTESLPNKYSTRVGDKGTQSLSGQKORIAIARALVRQPHIL 1200
DB 1134 RVVSQEEIVRAAKEANIHAFTESLPNKYSTRVGDKGTQSLSGQKORIAIARALVRQPHIL 1193
QY 1201 LDDEATSDALDTESEKVVQVQALDKARGRTTIVIAHRLSTIONADLIIVVONGVKEHGT 1260
DB 1194 LDDEATSDALDTESEKVVQVQALDKARGRTTIVIAHRLSTIONADLIIVVONGVKEHGT 1253
QY 1261 QQLLAQKGIYFSWVSQVQAGAKR 1282
DB 1254 QQLLAQKGIYFSWVSQVQAGAKR 1275

RESULT 4

DVS1

multidrug resistance protein 1 - mouse

N/Alternate names: P-glycoprotein 1

C/Species: Mus musculus (house mouse)

C/Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004

C/Accession: A33719; A25057; I57510

R/Raymond, M.; Gros, P.

Proc. Natl. Acad. Sci. U.S.A. 86, 6488-6492, 1989

A/Title: Mammalian multidrug-resistance gene: correlation of exon organization with str

A/Reference number: A33719; MUID:89367274; PMID:2570420

A/Accession: A33719

A/Molecule type: DNA

A/Residues: 1-1276 <RAY>

A/Cross-references: UNIPROT:P06795; UNIPARC:UPI00000210D8

R/Gros, P.; Croop, J.; Housman, D.

Cell 47, 371-380, 1986

A/Title: Mammalian multidrug resistance gene: complete cDNA sequence indicates strong h

A/Reference number: A25057; MUID:87028229; PMID:3768958

A/Accession: A25057

A/Molecule type: mRNA

A/Residues: 1-1276 <GRO>

DB 61 HGAGLPLMGLVFGDMTTFANAGNLGDLGALLFNNNTSSNITDTVPVNNLEEDMTRYAY 120
QY 118 YSGIGAGLVAAAYIQVSWFCLAGROTHKIRKQFFHAIHQEIGWFDVHDVGLNTRLTD 177
DB 121 YSGIGAGLVAAAYIQVSWFCLAGROTHKIRKQFFHAIHQEIGWFDVHDVGLNTRLTD 180
QY 178 DVSKINEGIDGKI GMPFQSMATPTFTGIVGTRGKLTIVLALSPVLGSAVAWAKILS 237
DB 181 DVSKINEGIDGKI GMPFQSMATPTFTGIVGTRGKLTIVLALSPVLGSAVAWAKILS 240
QY 238 SPTDKELLA YAKAGAAVEEVLAAIRTVIAFGGOKKELERNKLEAKRIGIKKATANI 297
DB 241 SPTDKELLA YAKAGAAVEEVLAAIRTVIAFGGOKKELERNKLEAKRIGIKKATANI 300
QY 298 SIGAFLIYASVALAFWYGTTLVLKSYISIGOVLTIVFVSVLIGAFSVGQASPSIEAFAN 357
DB 301 SIGAFLIYASVALAFWYGTTLVLKSYISIGOVLTIVFVSVLIGAFSVGQASPSIEAFAN 360
QY 358 ARGAAPEIKI IDNKPSIDSYSKSGHKPDNIKGNLEPRNVHFSYPSRKEVKILKGLNLKV 417
DB 361 ARGAAPEIKI IDNKPSIDSYSKSGHKPDNIKGNLEPRNVHFSYPSRKEVKILKGLNLKV 420
QY 418 QSGQTVLVGNSGCGKSTTVQLMORLYDPTGEMVSDGQDIRTINVRFLREIIGVYSQEP 477
DB 421 QSGQTVLVGNSGCGKSTTVQLMORLYDPTGEMVSDGQDIRTINVRFLREIIGVYSQEP 480
QY 478 VLPATTIAENIRYGREVDVMEIEKAVEANAYDFIMKLPQKFTDLVGERGAOLSGGQK 537
DB 481 VLPATTIAENIRYGREVDVMEIEKAVEANAYDFIMKLPQKFTDLVGERGAOLSGGQK 540
QY 538 RIAIARALVNPXKILLDEATSAIDTSEAVQVVALDKARKGRTTIVIAHRLSTVRNADV 597
DB 541 RIAIARALVNPXKILLDEATSAIDTSEAVQVVALDKARKGRTTIVIAHRLSTVRNADV 600
QY 598 IAGFDGVIYVEKGNHDELMKEGIIYFKLVMTQAGNIELENAADSKSIDTLEMSHD 657
DB 601 IAGFDGVIYVEKGNHDELMKEGIIYFKLVMTQAGNIELENAADSKSIDTLEMSHD 660
QY 658 SGSSLRKSTRSVRSGQODRKLTKEALDESIPVSWRIMKLNLTWPFVYGVVPC 717
DB 661 SGSSLRKSTRSVRSGQODRKLTKEALDESIPVSWRIMKLNLTWPFVYGVVPC 720
QY 718 AINGGLQAPAFVIFSKIIIGIFRNDDAETKRONSLFLLVLVIGVSPITFPFLOGFTF 777
DB 721 AINGGLQAPAFVIFSKIIIGIFRNDDAETKRONSLFLLVLVIGVSPITFPFLOGFTF 780
QY 778 GKAGEILTKELRYVWFVSMRQDVSWFDDPKNTTGALTTRLANDAAQVKGAGISRLAIT 837
DB 781 GKAGEILTKELRYVWFVSMRQDVSWFDDPKNTTGALTTRLANDAAQVKGAGISRLAIT 840
QY 838 QNTANLGTGIIISLIYQWLTLLLAIVPIIATAGVEMKLSGOALDKKKELEGAKIA 897
DB 841 QNTANLGTGIIISLIYQWLTLLLAIVPIIATAGVEMKLSGOALDKKKELEGAKIA 900
QY 898 TEAIENFRVTSITQEQFHEMDQSLQVPRNSLRKAHIFGTFSTQAMTFYVAGCF 957
DB 901 TEAIENFRVTSITQEQFHEMDQSLQVPRNSLRKAHIFGTFSTQAMTFYVAGCF 960
QY 958 RFQAYLVHSLMSEFEDVLLVFSVAVFGAMAVGVSSPAPYAKAKVSAAHIMIEKTPL 1017
DB 961 RFQAYLVHSLMSEFEDVLLVFSVAVFGAMAVGVSSPAPYAKAKVSAAHIMIEKTPL 1020
QY 1018 IDSYSYGLKPNTEGNTVNEVFNYPTRLDIPVLOGLSLEVKKGOTLALVSSGCGKS 1077
DB 1021 IDSYSYGLKPNTEGNTVNEVFNYPTRLDIPVLOGLSLEVKKGOTLALVSSGCGKS 1080
QY 1078 TVVQLLEFYDPLAGKVLGDKETIKOLNVQWLAHLGIVSQEPILFDCSISENIAYGDN 1137
DB 1081 TVVQLLEFYDPLAGKVLGDKETIKOLNVQWLAHLGIVSQEPILFDCSISENIAYGDN 1140
QY 1138 RVWSQEIIVRAAKENATHATIESLPNKYSTRVGDKGTQLSGGOKRIAIARALVROPHIL 1197
DB 1197 RVWSQEIIVRAAKENATHATIESLPNKYSTRVGDKGTQLSGGOKRIAIARALVROPHIL 1200

QY 1198 LLDEATSAIDTSEKVVQVQALDKARKGRTTIVIAHRLSTIQVADLIIVFQNGRVEKHGTH 1257
DB 1201 LLDEATSAIDTSEKVVQVQALDKARKGRTTIVIAHRLSTIQVADLIIVFQNGRVEKHGTH 1260
QY 1258 QOLLAOKGIYFSMVSVOAGAKRQ 1280
DB 1261 QOLLAOKGIYFSMVSVOAGAKRQ 1283
RESULT 6
ID AAW44073 standard protein; 1280 AA.
AC AAW44073;
XX
DT 25-MAR-2003 (revised)
DT 26-JUN-1998 (first entry)
XX Human multidrug resistance P-glycoprotein MDR1.
XX Human; multidrug resistance P-glycoprotein; MDR1; prokaryotic homologue.
XX Homo sapiens.
XX Key Location/Qualifiers
XX Region 1..640
FT /note= "MDR1-N from Fig 1"
FT Region 641..1280
FT /note= "MDR1-C from Fig 1"
XX WO9740160-A1.
XX 30-OCT-1997.
XX 24-APR-1997; 97WO-NO000216.
XX 24-APR-1996; 96EP-00201094.
XX (UYGR-) RIJTSUNIV GRONINGEN.
XX Van Veen HW, Venema K, Bolhuis H, Konings WN;
XX WPI; 1997-535844/49.
XX Prokaryotic homologue of human multiple drug resistance protein - used to
XX screen for compounds that inhibit, or avoid, drug resistance.
XX Claim 10; Fig 1; 35pp; English.
XX The present invention describes a recombinant or isolated nucleic acid
XX (I), derived from a prokaryotic gene, which encodes at least a specific
XX and/or functional part of a transporter protein (Tp), or its derivatives,
XX which has functional and/or structural similarity with the P-glycoprotein
XX (PG) encoded by the human multidrug resistance (MDR) 1 gene. The present
XX C as shown in the specification in figure 1. (I) is used to express
XX recombinant proteins; its fragments are also useful as probes and primers
XX for detection and amplification of related DNA. The protein produced, or
XX or avoid, MDR proteins, and in a screening method for identifying
XX compounds that inhibit transport of cytotoxic substances from cells.
XX Also, cells with a transmembrane protein, especially where expressed from
XX (I), can provide (additional) MDR, particularly for use as a model system
XX to study mechanisms of action of PG. (Updated on 25-MAR-2003 to correct
XX Pf field.)
XX Sequence 1280 AA;
SQ

Query Match 96.8%; Score 6218; DB 2; Length 1280;
Best Local Similarity 96.6%; Pred. No. 0;
Matches 1237; Conservative 19; Mismatches 24; Indels 0; Gaps 0;

QY 1 MDLEGRNGAECQKQNF FKLNNKS KDKCKKPTVSVFSPRYSNM LDKLYMVGTAAII 60
 Db 1 MDLEGRNGAECQKQNF FKLNNKS KDKCKKPTVSVFSPRYSNM LDKLYMVGTAAII 60
 QY 61 HGAGLPLMKLVFGDMTDTTANAGNLGDLGALLTNSNI TDTPVNNLEDMTRYAYTSG 120
 Db 61 HGAGLPLMKLVFGDMTDTTANAGNLGDLGALLTNSNI TDTPVNNLEDMTRYAYTSG 120
 QY 121 IGAGVLVAAYIOVSFWCLAAAGQIHKIRKQFFHAIMRQIOWDFVDHVGELNTRLTDDVS 180
 Db 121 IGAGVLVAAYIOVSFWCLAAAGQIHKIRKQFFHAIMRQIOWDFVDHVGELNTRLTDDVS 180
 QY 181 KINEGIGDKIGMFFOSMAFTFTGPIVGFTRGWKLTIVILAI SPVLGSLAAVWAKILSFT 240
 Db 181 KINEGIGDKIGMFFOSMAFTFTGPIVGFTRGWKLTIVILAI SPVLGSLAAVWAKILSFT 240
 QY 241 DKELIAYAKAGAVAEVLAAITVIAFGGKKLELYNKNLEAKRIGIKKAITANISIG 300
 Db 241 DKELIAYAKAGAVAEVLAAITVIAFGGKKLELYNKNLEAKRIGIKKAITANISIG 300
 QY 301 AAFILIIYASYALAFWYGTTLVLKSYSIGQVLTVPFSLVIGAFSVGQASPSIEAFANARG 360
 Db 301 AAFILIIYASYALAFWYGTTLVLKSYSIGQVLTVPFSLVIGAFSVGQASPSIEAFANARG 360
 QY 361 AAFILIIYASYALAFWYGTTLVLKSYSIGQVLTVPFSLVIGAFSVGQASPSIEAFANARG 420
 Db 361 AAFILIIYASYALAFWYGTTLVLKSYSIGQVLTVPFSLVIGAFSVGQASPSIEAFANARG 420
 QY 421 QTVLVGNSGCKSTTVQMLORLYDPTGWSVGDGDIINVRFLREIIGVVSEPVLF 480
 Db 421 QTVLVGNSGCKSTTVQMLORLYDPTGWSVGDGDIINVRFLREIIGVVSEPVLF 480
 QY 481 ATTIAENIRYGRDVTMDIEKAVKEANAYDFTMKLPQKFTLVGERGAQLSGGQKORIA 540
 Db 481 ATTIAENIRYGRDVTMDIEKAVKEANAYDFTMKLPQKFTLVGERGAQLSGGQKORIA 540
 QY 541 IARALVRNPKIILLDEATSEALDTESEAVVOVALDKARKORTTIVIAHRLSTVRNADVIAG 600
 Db 541 IARALVRNPKIILLDEATSEALDTESEAVVOVALDKARKORTTIVIAHRLSTVRNADVIAG 600
 QY 601 PDGQVIVKGNDELKMKGIYFKLVTMTAGNEIELENADESKSEIDTLEMSHDSGS 660
 Db 601 PDGQVIVKGNDELKMKGIYFKLVTMTAGNEIELENADESKSEIDTLEMSHDSGS 660
 QY 661 SLIRKSTRSRVSGSQDRKLSKEALDESIPVSVFWRIMKMLNLTWPYFVGVFCAII 720
 Db 661 SLIRKSTRSRVSGSQDRKLSKEALDESIPVSVFWRIMKMLNLTWPYFVGVFCAII 720
 QY 721 NGGLQAPAFVFSKIIGITFRNDDAETKRONSLFSLLLFLVLGIVSFITPFLQGFPGA 780
 Db 721 NGGLQAPAFVFSKIIGITFRNDDAETKRONSLFSLLLFLVLGIVSFITPFLQGFPGA 780
 QY 781 GELTLKRLRVWFRSMLRQDVSPDFDPTNTGALTTRLANDAAQVKGAGSLRAITONI 840
 Db 781 GELTLKRLRVWFRSMLRQDVSPDFDPTNTGALTTRLANDAAQVKGAGSLRAITONI 840
 QY 841 ANLGTGIIISLIYGWOLTLALLAIVPIIAIAGVVMKMLSGQALDKKKELEGAGKIATEA 900
 Db 841 ANLGTGIIISLIYGWOLTLALLAIVPIIAIAGVVMKMLSGQALDKKKELEGAGKIATEA 900
 QY 901 IENFRVTVSLTQOKFHEMTDQSLQVPRNSLRKAHFGITFTQNTQMMYFVAGCFRFG 960
 Db 901 IENFRVTVSLTQOKFHEMTDQSLQVPRNSLRKAHFGITFTQNTQMMYFVAGCFRFG 960
 QY 961 AYLVAHSLMFEDVLLVFSVAFGMAVGVSPADYAKAVSAHHIMIEKTPILDS 1020
 Db 961 AYLVAHSLMFEDVLLVFSVAFGMAVGVSPADYAKAVSAHHIMIEKTPILDS 1020
 QY 1021 YSTEGLKPNLTLEGNTVFNWVFNPTPLDIPVLQGLSLEVKKGQTLALVSGSGCKSTTV 1080
 Db 1021 YSTEGLKPNLTLEGNTVFNWVFNPTPLDIPVLQGLSLEVKKGQTLALVSGSGCKSTTV 1080
 QY 1081 QLLERFYDPLAGKVLDDKKEIKQLNVQWLAHGLIVSQEPIILPDCSISENIAYGDSRVV 1140

Db 1081 QLLERFYDPLAGKVLDDKKEIKQLNVQWLAHGLIVSQEPIILPDCSISENIAYGDSRVV 1140
 QY 1141 SQEEIVRAAKEANIHAIFIESLPNKYSTRVGDKGTQLSGGQKORIAIARALVRQPHILLD 1200
 Db 1141 SQEEIVRAAKEANIHAIFIESLPNKYSTRVGDKGTQLSGGQKORIAIARALVRQPHILLD 1200
 QY 1201 EATSALDTESEKVOEALDKARGRTCTIVIAHRLSTIQTADLIIVFONGRVKHEGTHQOL 1260
 Db 1201 EATSALDTESEKVOEALDKARGRTCTIVIAHRLSTIQTADLIIVFONGRVKHEGTHQOL 1260
 QY 1261 LAQKGIYFSMVSVQAGAKRQ 1280
 Db 1261 LAQKGIYFSMVSVQAGAKRQ 1280
 RESULT 7
 AAY58186
 ID AAY58186 standard; protein; 1280 AA.
 XX AC AAY58186;
 XX 14-MAR-2000 (first entry)
 XX Human wild-type multidrug resistance-1 (MDR-1) protein.
 DE Multidrug resistance; MDR-1; P-glycoprotein; transmembrane efflux pump;
 KW haematopoietic stem cell; transduction; bone marrow transplantation;
 KW chemotherapy; radiation therapy; cancer; gene therapy; gene replacement;
 KW genetic defect; thalasassaemia; Gauchier's disease; sickle cell anaemia;
 KW leukaemia; ex vivo expansion; cytokine; wild-type.
 XX Homo sapiens.
 OS
 XX
 FH Key
 FT Misc-difference 185
 FT /note= "This residue is Val in a mutant MDR-1 (AAY58187)".
 XX
 XX
 XX WO9961589-A2.
 XX
 XX 02-DEC-1999.
 XX 27-MAY-1999; 99WO-US011825.
 XX 28-MAY-1998; 98US-0086988P.
 XX (SJUD-) ST JUDE CHILDREN'S RES HOSPITAL.
 XX Sorrentino B, Bunting K;
 XX WPI; 2000-072615/06.
 XX N-PSDB; AAZ49332.
 XX Ex vivo expansion of hematopoietic stem cells transduced with a sequence
 PT encoding human multidrug resistance-1, used for bone marrow
 PT transplantation.
 XX Claim 10; Page 71-79; 113pp; English.
 XX This sequence represents human wild-type multidrug resistance protein MDR
 CC -1. MDR-1 is a transmembrane efflux pump, responsible for the export of
 CC drugs from certain cells, particularly cancer cells. Wild-type MDR-1
 CC shows increased resistance to etoposide and decreased resistance to vinca
 CC alkaloids compared with a mutant form (AAY58187) where the Gly at
 CC position 185 is replaced by Val. The invention relates to transducing
 CC haematopoietic stem cells with nucleic acid encoding an MDR protein and
 CC culturing the modified cells. The modified haematopoietic stem cells are
 CC useful in bone marrow transplantation (to reconstitute haematopoietic
 CC systems in patients who have undergone chemotherapy or radiation therapy)
 CC and in ex vivo gene therapy of genetic defects in cells derived from
 CC haematopoietic stem cells, e.g., thalasassaemia, Gauchier's disease, sickle
 CC cell anaemia or leukaemia. The modified cells can also be used to
 CC identify factors involved in regulating proliferation and differentiation

Query Match	96.6%; Score 6209; DB 2; Length 1280;	
Best Local Similarity	96.6%; Pred. No. 0;	
Matches 1236; Conservative	19; Mismatches 25; Indels 0; Gaps 0;	
QY	1 MDLEGRNGAEKKNFFKLNKSKDKCKRKPVTVSFMSFRYSNWLDKLVMVGTAAII	60
DB	1 MDLEGRNGAKKCNFFKLNKSEKCKEKKPTVSFMSFRYSNWLDKLVMVGTAAII	60
QY	61 HGAGLPLMLVFGDMTDPANAGNLGDLGALLTNSNITDTPVPMLEEDMTYATYISG	120
DB	61 HGAGLPLMLVFGEMTDPANAGNLEDLMSNITNRSNDINDTGFPMLEEDMTYATYISG	120
QY	121 IGAGLVAAIYQVSFWCLAAAGROIHKIRKQFFHAIIMRQEIQWDFVDVHDELNLTDDVS	180
DB	121 IGAGLVAAIYQVSFWCLAAAGROIHKIRKQFFHAIIMRQEIQWDFVDVHDELNLTDDVS	180
QY	181 KINEGIGDKIGMFFQSMATFPTGFTVGTGKWLTLVLAISPVLGLSAAVWAKILSSFT	240
DB	181 KINEVIGDKIGMFFQSMATFPTGFTVGTGKWLTLVLAISPVLGLSAAVWAKILSSFT	240
QY	241 DKELLAYAKAGAAVEVLAIRTVIAGGOKKELRYNKNLEAKRIGIKKAITANISIG	300
DB	241 DKELLAYAKAGAAVEVLAIRTVIAGGOKKELRYNKNLEAKRIGIKKAITANISIG	300
QY	301 APELLIYASVALAFVGTTLVLSEYSIGQVLTFFSVLIGAFSGVQASPIEAFANARG	360
DB	301 APELLIYASVALAFVGTTLVLSEYSIGQVLTFFSVLIGAFSGVQASPIEAFANARG	360
QY	361 AAFBEIKIINPKSIDSYSGHKKPNKGNLEFRNVHFSYPSRKEVKILKGLNLKQVSG	420
DB	361 ANVEIFKLIINPKSIDSYSGHKKPNKGNLEFRNVHFSYPSRKEVKILKGLNLKQVSG	420
QY	421 QTVLVNCSGCGKSTTVQLMORLVDPTEGMVSDGQDRTINVRFLREIIGVSWQEVLF	480
DB	421 QTVLVNCSGCGKSTTVQLMORLVDPTEGMVSDGQDRTINVRFLREIIGVSWQEVLF	480
QY	481 ATTAEINIRGREVDVDETEKAVEANAVDFIMKLPKPTLVGERGAOLSGQKORIA	540
DB	481 ATTAEINIRGREVDVDETEKAVEANAVDFIMKLPKPTLVGERGAOLSGQKORIA	540
QY	541 IARALVRNPKILLDEATSDALDTESEAVQVVALDKARKGRTTIVIAHRLSTVRNADVIAG	600
DB	541 IARALVRNPKILLDEATSDALDTESEAVQVVALDKARKGRTTIVIAHRLSTVRNADVIAG	600
QY	601 FDDGVIIVEKGNHDELMEKGIYFKLVMTQAGNEIENADESKSEIDTLEMSHDSGS	660
DB	601 FDDGVIIVEKGNHDELMEKGIYFKLVMTQAGNEIENADESKSEIDALEMSHDSRS	660
QY	661 SLIRKSTRSRVSGSQDRKLSKEALDSEIIPVSVFWIRIMKLNLTWPPVFWVGVFCALI	720
DB	661 SLIRKSTRSRVSGSQDRKLSKEALDSEIIPVSVFWIRIMKLNLTWPPVFWVGVFCALI	720
QY	721 NGGLQPAFAVIFSKIIIGIFTRNDDAETKRONSLFSLFLVLGIVSFITPFLQFTGKA	780
DB	721 NGGLQPAFAVIFSKIIIGIFTRNDDAETKRONSLFSLFLALGIIISFITPFLQFTGKA	780
QY	781 GEILTKELRYNVRFSMLRQDVSFDDPKNTTGALTTRLANDAAQVKGAIKSLAIITONI	840
DB	781 GEILTKELRYNVRFSMLRQDVSFDDPKNTTGALTTRLANDAAQVKGAIKSLRLAVITONI	840
QY	841 ANLGTGIIISLIGWQLTLLALLAIVPIIAIAGVEMKMLSGQALKDKKELESGAGKIATEA	900
DB	841 ANLGTGIIISPIYQWLTLLALLAIVPIIAIAGVEMKMLSGQALKDKKELESGAGKIATEA	900
QY	901 IENPRTVVSLSLTOEQKFEHMDQSLQVPRNSLRKAHIFGIFTSFTQAMWYSYACGRFPG	960
DB	901 IENPRTVVSLSLTOEQKFEHMAQSLQVPRNSLRKAHIFGIFTSFTQAMWYSYACGRFPG	960
QY	961 AYLVAHSLMSPEDVLLVFSVAVFGAMAVQVSSPAPDYAKAVSAHIIIMIIETPLIDS	1020
DB	961 AYLVAHSLMSPEDVLLVFSVAVFGAMAVQVSSPAPDYAKAKISAHIIIMIIETPLIDS	1020
QY	1021 YSTGLKPNLTLEGNVTFEUVNPTRPDIIPVLOGLSLEVKKGTTLALVSGSGCGKSTVV	1080

DB	1021 YSTGLKPNLTLEGNVTFEUVNPTRPDIIPVLOGLSLEVKKGTTLALVSGSGCGKSTVV	1080
QY	1081 QLLERFYDPLAGKVLDDGKEIKOLNVQWLAHGLTVSOEPIILFDCSISENIAYGDSRVV	1140
DB	1081 QLLERFYDPLAGKVLDDGKEIKRLNVQWLAHGLTVSOEPIILFDCSIAENIAYGDSRVV	1140
QY	1141 SOEETVRAAKENIAHAFIESLPNKYSTYRVDKGTOLSGQKORIAIARALVRPHILLD	1200
DB	1141 SOEETVRAAKENIAHAFIESLPNKYSTYRVDKGTOLSGQKORIAIARALVRPHILLD	1200
QY	1201 EATSALDTESEKVOEALDKAREGTCIVIAHRLSTIONADLIVVFGNVRKVEHGHQOOL	1260
DB	1201 EATSALDTESEKVOEALDKAREGTCIVIAHRLSTIONADLIVVFGNVRKVEHGHQOOL	1260
QY	1261 LAQKGIYFSMVSVOAGAKRQ	1280
DB	1261 LAQKGIYFSMVSVOAGTKRQ	1280

RESULT 11

US-09-817-762-3

Sequence 3, Application US/09817762

Patent No. 6886774

GENERAL INFORMATION:

APPLICANT: Spalding, Edgar P.

APPLICANT: No. 6858774, Bosl

TITLE OF INVENTION: MDR-Like ABC Transporter Gene From

TITLE OF INVENTION: Plants

FILE REFERENCE: 13238-00061

CURRENT APPLICATION NUMBER: US/09/817,762

CURRENT FILING DATE: 2001-03-26

PRIOR APPLICATION NUMBER: PCT/US99/22363

PRIOR FILING DATE: 1999-09-24

PRIOR APPLICATION NUMBER: US 60/101,814

PRIOR FILING DATE: 1998-09-25

NUMBER OF SEQ ID NOS: 14

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 3

LENGTH: 1280

TYPE: PRT

ORGANISM: Homo sapiens

PUBLICATION INFORMATION:

DATABASE ACCESSION NUMBER: Genbank P08183

DATABASE ENTRY DATE: 1997-11-01

US-09-817-762-3

Query Match 96.6%; Score 6209; DB 2; Length 1280;

Best Local Similarity 96.6%; Pred. No. 0;

Matches 1236; Conservative 19; Mismatches 25; Indels 0; Gaps 0;

QY 1 MDLEGRNGAEKKNFFKLNKSKDKCKRKPVTVSFMSFRYSNWLDKLVMVGTAAII 60

DB 1 MDLEGRNGAKKCNFFKLNKSEKCKEKKPTVSFMSFRYSNWLDKLVMVGTAAII 60

QY 61 HGAGLPLMLVFGDMTDPANAGNLGDLGALLTNSNITDTPVPMLEEDMTYATYISG 120

DB 61 HGAGLPLMLVFGEMTDPANAGNLEDLMSNITNRSNDINDTGFPMLEEDMTYATYISG 120

QY 121 IGAGLVAAIYQVSFWCLAAAGROIHKIRKQFFHAIIMRQEIQWDFVDVHDELNLTDDVS 180

DB 121 IGAGLVAAIYQVSFWCLAAAGROIHKIRKQFFHAIIMRQEIQWDFVDVHDELNLTDDVS 180

QY 181 KINEGIGDKIGMFFQSMATFPTGFTVGTGKWLTLVLAISPVLGLSAAVWAKILSSFT 240

DB 181 KINEVIGDKIGMFFQSMATFPTGFTVGTGKWLTLVLAISPVLGLSAAVWAKILSSFT 240

QY 241 DKELLAYAKAGAAVEVLAIRTVIAGGOKKELRYNKNLEAKRIGIKKAITANISIG 300

DB 241 DKELLAYAKAGAAVEVLAIRTVIAGGOKKELRYNKNLEAKRIGIKKAITANISIG 300

QY 301 APELLIYASVALAFVGTTLVLSEYSIGQVLTFFSVLIGAFSGVQASPIEAFANARG 360

DB 301 APELLIYASVALAFVGTTLVLSEYSIGQVLTFFSVLIGAFSGVQASPIEAFANARG 360

QY 361 AAFBEIKIINPKSIDSYSGHKKPNKGNLEFRNVHFSYPSRKEVKILKGLNLKQVSG 420

DB 361 ANVEIFKLIINPKSIDSYSGHKKPNKGNLEFRNVHFSYPSRKEVKILKGLNLKQVSG 420

QY 421 QTVLVNCSGCGKSTTVQLMORLVDPTEGMVSDGQDRTINVRFLREIIGVSWQEVLF 480

DB 421 QTVLVNCSGCGKSTTVQLMORLVDPTEGMVSDGQDRTINVRFLREIIGVSWQEVLF 480

QY 481 ATTAEINIRGREVDVDETEKAVEANAVDFIMKLPKPTLVGERGAOLSGQKORIA 540

DB 481 ATTAEINIRGREVDVDETEKAVEANAVDFIMKLPKPTLVGERGAOLSGQKORIA 540

QY 541 IARALVRNPKILLDEATSDALDTESEAVQVVALDKARKGRTTIVIAHRLSTVRNADVIAG 600

DB 541 IARALVRNPKILLDEATSDALDTESEAVQVVALDKARKGRTTIVIAHRLSTVRNADVIAG 600

QY 601 FDDGVIIVEKGNHDELMEKGIYFKLVMTQAGNEIENADESKSEIDTLEMSHDSGS 660

DB 601 FDDGVIIVEKGNHDELMEKGIYFKLVMTQAGNEIENADESKSEIDALEMSHDSRS 660

QY 661 SLIRKSTRSRVSGSQDRKLSKEALDSEIIPVSVFWIRIMKLNLTWPPVFWVGVFCALI 720

DB 661 SLIRKSTRSRVSGSQDRKLSKEALDSEIIPVSVFWIRIMKLNLTWPPVFWVGVFCALI 720

QY 721 NGGLQPAFAVIFSKIIIGIFTRNDDAETKRONSLFSLFLVLGIVSFITPFLQFTGKA 780

DB 721 NGGLQPAFAVIFSKIIIGIFTRNDDAETKRONSLFSLFLALGIIISFITPFLQFTGKA 780

QY 781 GEILTKELRYNVRFSMLRQDVSFDDPKNTTGALTTRLANDAAQVKGAIKSLAIITONI 840

DB 781 GEILTKELRYNVRFSMLRQDVSFDDPKNTTGALTTRLANDAAQVKGAIKSLRLAVITONI 840

QY 841 ANLGTGIIISLIGWQLTLLALLAIVPIIAIAGVEMKMLSGQALKDKKELESGAGKIATEA 900

DB 841 ANLGTGIIISPIYQWLTLLALLAIVPIIAIAGVEMKMLSGQALKDKKELESGAGKIATEA 900

QY 901 IENPRTVVSLSLTOEQKFEHMDQSLQVPRNSLRKAHIFGIFTSFTQAMWYSYACGRFPG 960

DB 901 IENPRTVVSLSLTOEQKFEHMAQSLQVPRNSLRKAHIFGIFTSFTQAMWYSYACGRFPG 960

QY 961 AYLVAHSLMSPEDVLLVFSVAVFGAMAVQVSSPAPDYAKAVSAHIIIMIIETPLIDS 1020

DB 961 AYLVAHSLMSPEDVLLVFSVAVFGAMAVQVSSPAPDYAKAKISAHIIIMIIETPLIDS 1020

QY 1021 YSTGLKPNLTLEGNVTFEUVNPTRPDIIPVLOGLSLEVKKGTTLALVSGSGCGKSTVV 1080

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 361 AAFIFIKIDNKPSIDSKSGHKPDNKGMLFRNVHPSYPSRKEVKILKGLNLKXVQSG 420
 361 AAYEIFIKIDNKPSIDSKSGHKPDNKGMLFRNVHPSYPSRKEVKILKGLNLKXVQSG 420
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 421 QTVALVNSGCGKSTTVQLMORLYDPTGEMVSDGQDRTINVRFLREIIGVVSQEPVLF 480
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 541 IARALVRNPKILLDEATSDALDTESEAVVQVALDKARKGRITIVIAHRLSTVRNADVIAG 600
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 601 FDDGVIVEKGNHDELMEKGIYFKLVMTQTAGNEIELENAADESKSEIDTLEMSSHDGSGS 660
 601 FDDGVIVEKGNHDELMEKGIYFKLVMTQTAGNEIELENAADESKSEIDTLEMSSHDGSGS 660
 661 SLIRKSTRSRVRSQGDRLKSTKEALDESIIPVSVFWRIMKLNLTWPFYVGVFCALI 720
 661 SLIRKSTRSRVRSQGDRLKSTKEALDESIIPVSVFWRIMKLNLTWPFYVGVFCALI 720
 721 NGGLQPAFAVTFSKIIGITFTRNDDAETKRONSLFSLFLVLGIVSPITTFPLOGFTFGKA 780
 721 NGGLQPAFAVTFSKIIGITFTRNDDAETKRONSLFSLFLVLGIVSPITTFPLOGFTFGKA 780
 781 GEILTKLRYVFRSMRLQDVSFDDPNTTGALTTRLANDAAQVKGAGISRLAITONI 840
 781 GEILTKLRYVFRSMRLQDVSFDDPNTTGALTTRLANDAAQVKGAGISRLAITONI 840
 841 ANLGTGIIISLYGWLTLALLAIVPIIAIAGVEMKMLSGOALKKKELEGACKIATEA 900
 841 ANLGTGIIISLYGWLTLALLAIVPIIAIAGVEMKMLSGOALKKKELEGACKIATEA 900
 901 IENFTVVSLLTOEQKFEHMYDQSLQVYPYNSLRKAHIFGIFTFSTQAMWYFSYAGCFRFG 960
 901 IENFTVVSLLTOEQKFEHMYDQSLQVYPYNSLRKAHIFGIFTFSTQAMWYFSYAGCFRFG 960
 961 AYLVAHMSFEDVLLVFSVAVFGAMAVGVSSFAPDYAKAVKVAASHIIMIEKTPLIDS 1020
 961 AYLVAHMSFEDVLLVFSVAVFGAMAVGVSSFAPDYAKAVKVAASHIIMIEKTPLIDS 1020
 1021 YSTGLKENTILEGNVTFNEVVPYPTRLDIPVLQGLSLEVKKGOTLALVSGSGCGKSTVV 1080
 1021 YSTGLKENTILEGNVTFNEVVPYPTRLDIPVLQGLSLEVKKGOTLALVSGSGCGKSTVV 1080
 1081 QLLERFYDPLAGKVLDDGKEIKQLNVOLRAHLGIVSQEPILFDCSISENIAYGDNRRV 1140
 1081 QLLERFYDPLAGKVLDDGKEIKQLNVOLRAHLGIVSQEPILFDCSISENIAYGDNRRV 1140
 1141 SQEIVRAAKANHAFTESLPNKYSTVGVKGTQSGQKORIAIARALVRPHILLD 1200
 1141 SQEIVRAAKANHAFTESLPNKYSTVGVKGTQSGQKORIAIARALVRPHILLD 1200
 1201 EATSALDTESEKVVQEALDKAREGTCIVIAHRLSTIONADLIIVFQNGRVEKHGTHOOL 1260
 1201 EATSALDTESEKVVQEALDKAREGTCIVIAHRLSTIONADLIIVFQNGRVEKHGTHOOL 1260
 1261 LAQKGIYFSMVSVQAGAKRQ 1280
 1261 LAQKGIYFSMVSVQAGAKRQ 1280

RESULT 12
 US-09-584-586-4
 ; Sequence 4, Application US/09584586
 ; Patent No: 693150
 ; GENERAL INFORMATION:
 ; APPLICANT: Sorrentino, Brian

APPLICANT: Bunting, Kevin
 TITLE OF INVENTION: EXPANSION OF HEMATOPOIETIC STEM CELLS TRANSDUCED WITH
 FILE REFERENCE: MDR-1 METHODS OF USE THEREOF
 CURRENT APPLICATION NUMBER: US/09/584,586
 CURRENT FILING DATE: 2000-05-31
 EARLIER APPLICATION NUMBER: US 60/086,988
 EARLIER FILING DATE: 1998-05-28
 EARLIER APPLICATION NUMBER: PCT/US99/11825
 EARLIER FILING DATE: 1999-05-27
 NUMBER OF SEQ ID NOS: 16
 SOFTWARE: Patent in Ver. 2.0
 SEQ ID NO 4
 LENGTH: 1280
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 OTHER INFORMATION: Human MDR 185-V
 US-09-584-586-4

Query Match 96.6%; Score 6209; DB 2; Length 1280;
 Best Local Similarity 96.6%; Pred. No. 0;
 Matches 1236; Conservative 19; Mismatches 25; Indels 0; Gaps 0;

Qy 1 MDLEGDRNGAEGKGNPFKLNKSKKKKPKPTVSFMSFRYSNWLDKLYMVVGTLLAAII 60
 Db 1 MDLEGDRNGAEGKGNPFKLNKSKKKKPKPTVSFMSFRYSNWLDKLYMVVGTLLAAII 60
 Qy 61 HGAGLPLMLVFGDMTDTFANAGNLGDLGALLTNSNITDTVPVNMLEEDTRYAYYSG 120
 Db 61 HGAGLPLMLVFGDMTDTFANAGNLGDLGALLTNSNITDTVPVNMLEEDTRYAYYSG 120
 Qy 121 IGAGLVAAIYQVSPFCLAAAGROHKKQPHAIHQISGFWDFHVDVCELNRLTDDVS 180
 Db 121 IGAGLVAAIYQVSPFCLAAAGROHKKQPHAIHQISGFWDFHVDVCELNRLTDDVS 180
 Qy 181 KINEGIDKIMGFQSMATFTFTGIVGFTGKWLTLVILAIAPVLGLSAVWAKILSSFT 240
 Db 181 KINEGIDKIMGFQSMATFTFTGIVGFTGKWLTLVILAIAPVLGLSAVWAKILSSFT 240
 Qy 241 DKELLAYAKAGAVAEVLAARTVIAFGGOKKELRYNKNLEAKGIGIKAITANISIG 300
 Db 241 DKELLAYAKAGAVAEVLAARTVIAFGGOKKELRYNKNLEAKGIGIKAITANISIG 300
 Qy 301 AAFLLIYASYALAFWYGTTLVLGSEYSGVLTVPFVSLGAPSVGQASPSIEAFANARG 360
 Db 301 AAFLLIYASYALAFWYGTTLVLGSEYSGVLTVPFVSLGAPSVGQASPSIEAFANARG 360
 Qy 361 AAFIPIKIDNKPSIDSKSGHKPDNKGMLFRNVHPSYPSRKEVKILKGLNLKXVQSG 420
 Db 361 AAFIPIKIDNKPSIDSKSGHKPDNKGMLFRNVHPSYPSRKEVKILKGLNLKXVQSG 420
 Qy 421 QTVALVNSGCGKSTTVQLMORLYDPTGEMVSDGQDRTINVRFLREIIGVVSQEPVLF 480
 Db 421 QTVALVNSGCGKSTTVQLMORLYDPTGEMVSDGQDRTINVRFLREIIGVVSQEPVLF 480
 Qy 481 ATTIAENIRYGRDVTWDEIEKAVKEANAYDFIMKLPOKFTDLVGERGAQLSGGQKORIA 540
 Db 481 ATTIAENIRYGRDVTWDEIEKAVKEANAYDFIMKLPOKFTDLVGERGAQLSGGQKORIA 540
 Qy 541 IARALVRNPKILLDEATSDALDTESEAVVQVALDKARKGRITIVIAHRLSTVRNADVIAG 600
 Db 541 IARALVRNPKILLDEATSDALDTESEAVVQVALDKARKGRITIVIAHRLSTVRNADVIAG 600
 Qy 601 FDDGVIVEKGNHDELMEKGIYFKLVMTQTAGNEIELENAADESKSEIDTLEMSSHDGSGS 660
 Db 601 FDDGVIVEKGNHDELMEKGIYFKLVMTQTAGNEIELENAADESKSEIDTLEMSSHDGSGS 660
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 Db 661 SLIRKSTRSRVRSQGDRLKSTKEALDESIIPVSVFWRIMKLNLTWPFYVGVFCALI 720
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Db 721 NGGLQAPAFIFSKIIIGVTRIDDPETKRONSLFSLFLALGIIISFITFFLQGTFGKA 780
Qy 781 GEILTKRLRYMVFRLQDVSFDDPKNTTGATLRLANDAAQVKGAGISRLAIIQNI 840
Db 781 GEILTKRLRYMVFRLQDVSFDDPKNTTGATLRLANDAAQVKGAGISRLAIIQNI 840
Qy 841 ANLGTGIIISIIYHQLTLLIIAIVPIIAIGVEMKMLSGQALKDKKELEGAGKATEA 900
Db 841 ANLGTGIIISIIYHQLTLLIIAIVPIIAIGVEMKMLSGQALKDKKELEGAGKATEA 900
Qy 901 IENERTVVSUTQOBKFEHMYDQSLQVPRNSLRKAHIFGITPSTQAMVFSYACGCRFG 960
Db 901 IENERTVVSUTQOBKFEHMYDQSLQVPRNSLRKAHIFGITPSTQAMVFSYACGCRFG 960
Qy 961 AYLVHSLMSPEDVLLVFSVAVFGAMAVQVSSFAPDYAKAKVSAHIIIMIEKTPLIDS 1020
Db 961 AYLVHSLMSPEDVLLVFSVAVFGAMAVQVSSFAPDYAKAKVSAHIIIMIEKTPLIDS 1020
Qy 1021 YSTEGLKPNTEGNTVEVFNYPTRDIPVLAQLSLEVKKGOTLALVSSGCGKSTVV 1080
Db 1021 YSTEGLKPNTEGNTVEVFNYPTRDIPVLAQLSLEVKKGOTLALVSSGCGKSTVV 1080
Qy 1081 QLLERFVDPVLAGKVLIDGKEIKOLNVOWLRAHLGIVSQEPILFDCSISENIAIYDNRV 1140
Db 1081 QLLERFVDPVLAGKVLIDGKEIKOLNVOWLRAHLGIVSQEPILFDCSISENIAIYDNRV 1140
Qy 1141 SOBEIVRAAKANIHAFIESLPNKYSTVGDKTQSGGQKQRIATARALVRPHILLD 1200
Db 1141 SOBEIVRAAKANIHAFIESLPNKYSTVGDKTQSGGQKQRIATARALVRPHILLD 1200
Qy 1201 EATSALDTESEKVOBALDKAREGTCIVIAHRLSTIQNADLIIVFQNGRVEKHGTHQOL 1260
Db 1201 EATSALDTESEKVOBALDKAREGTCIVIAHRLSTIQNADLIIVFQNGRVEKHGTHQOL 1260
Qy 1261 LAQKGIYFMSVSVQAGAKRQ 1280
Db 1261 LAQKGIYFMSVSVQAGAKRQ 1280

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RESULT 13
US-08-583-276-19
; Sequence 19, Application US/08583276
; Patent No. 5837536
; GENERAL INFORMATION:
; APPLICANT: McDonagh, Kevin T.
; APPLICANT: Nienhuis, Arthur
; TITLE OF INVENTION: IMPROVED EXPRESSION OF HUMAN
; TITLE OF INVENTION: MULTIDRUG RESISTANCE GENES AND IMPROVED
; TITLE OF INVENTION: SELECTION OF CELLS TRANSDUCED WITH SUCH GENES
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESS: Carella, Byrns, Bain, Gilfillan,
; ADDRESS: Cecchi & Stewart
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: DW4.V2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/583,276
; FILING DATE: 05-JAN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/332,444
; FILING DATE: 31-OCT-1994
; APPLICATION NUMBER: 07/887,712

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; FILING DATE: 22-MAY-1992
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1280 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: protein
; US-08-583-276-19

Query Match 96.6%; Score 6206; DB 1; Length 1280;
Best Local Similarity 96.5%; Pred. No. 0;
Matches 1235; Conservative 20; Mismatches 25; Indels 0; Gaps 0;

Qy 1 MDLEGRNKGAEKKNPFKLNKSKDKKPKPTVSVPMSRYSNWLDKLYMVVGTLLAAII 60
Db 1 MDLEGRNKGAEKKNPFKLNKSKDKKPKPTVSVPMSRYSNWLDKLYMVVGTLLAAII 60
Qy 61 HGAGLPMLLVFGDMTDTFANAGNLGDLGALLTNSNITDTVPVNMLEDMDTRYAYYSG 120
Db 61 HGAGLPMLLVFGDMTDTFANAGNLGDLGALLTNSNITDTVPVNMLEDMDTRYAYYSG 120
Qy 121 IGAGVLVAAYIOVSFWCLAAAGRIHKIRKQFPHAIMROEIGWFDVHDVGEINLRLTDDVS 180
Db 121 IGAGVLVAAYIOVSFWCLAAAGRIHKIRKQFPHAIMROEIGWFDVHDVGEINLRLTDDVS 180
Qy 181 KNEGIGDKIGMFPFOSMATFFTFGIVGTRGKCLTLVILAIISPVLGLSAAVWAKILSSFT 240
Db 181 KNEGIGDKIGMFPFOSMATFFTFGIVGTRGKCLTLVILAIISPVLGLSAAVWAKILSSFT 240
Qy 241 DKELLAYAKAGAAVEVLAAITVTIAGGQKKELEKRYNKNLEAKRIGIKKAITANISIG 300
Db 241 DKELLAYAKAGAAVEVLAAITVTIAGGQKKELEKRYNKNLEAKRIGIKKAITANISIG 300
Qy 301 AAFLLIYASIALAFWYGTTLVLSKEYSIGQVLTVPFVSVLIGAFSGVQASPSIEAFANARG 360
Db 301 AAFLLIYASIALAFWYGTTLVLSKEYSIGQVLTVPFVSVLIGAFSGVQASPSIEAFANARG 360
Qy 361 AAFEIFKIIDNKPSIDSYKSGHKPDNKGLEFRNVHFSYPSRKEVKILKGLNKVQSG 420
Db 361 AAFEIFKIIDNKPSIDSYKSGHKPDNKGLEFRNVHFSYPSRKEVKILKGLNKVQSG 420
Qy 421 QTVALVNGSGCGKSTTVQLMQRLYDPTBGMVSVVDQDITRTINVRFLREIIGVVSQEPVLF 480
Db 421 QTVALVNGSGCGKSTTVQLMQRLYDPTBGMVSVVDQDITRTINVRFLREIIGVVSQEPVLF 480
Qy 481 ATTIAENIRYGRVDVTHMDEIEKAVKEANAYDFIMKLPOKPTLVGERGAQLSGGQKORIA 540
Db 481 ATTIAENIRYGRVDVTHMDEIEKAVKEANAYDFIMKLPOKPTLVGERGAQLSGGQKORIA 540
Qy 541 IARALVRNPKILLDEATSAIDTSEAVVVALDKARKGRITIVIAHRLSTVRNADVIAG 600
Db 541 IARALVRNPKILLDEATSAIDTSEAVVVALDKARKGRITIVIAHRLSTVRNADVIAG 600
Qy 601 PDDGVIVKGNHDELMKEKGIYFKLVMTQAGNEIELENAADESKSIDTLEMSSHDSGS 660
Db 601 PDDGVIVKGNHDELMKEKGIYFKLVMTQAGNEIELENAADESKSIDTLEMSSHDSGS 660
Qy 661 SLIKRSTRSRVSGSQDRLSTKEALDESIIPVSWRIMKLNLTWPYFVGVFCALII 720
Db 661 SLIKRSTRSRVSGSQDRLSTKEALDESIIPVSWRIMKLNLTWPYFVGVFCALII 720
Qy 721 NGGLQAPAFIFSKIIIGVTRIDDPETKRONSLFSLFLALGIIISFITFFLQGTFGKA 780
Db 721 NGGLQAPAFIFSKIIIGVTRIDDPETKRONSLFSLFLALGIIISFITFFLQGTFGKA 780
Qy 781 GEILTKRLRYMVFRLQDVSFDDPKNTTGATLRLANDAAQVKGAGISRLAIIQNI 840
Db 781 GEILTKRLRYMVFRLQDVSFDDPKNTTGATLRLANDAAQVKGAGISRLAIIQNI 840
Qy 841 ANLGTGIIISIIYHQLTLLIIAIVPIIAIGVEMKMLSGQALKDKKELEGAGKATEA 900
Db 841 ANLGTGIIISIIYHQLTLLIIAIVPIIAIGVEMKMLSGQALKDKKELEGAGKATEA 900

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Db 841 ANLGTGIIISPIYCHQTLTLLLAIVPIIATAGVVMKLSGQALXDKKELEGAGKIATEA 900
Qy 901 IENFRTVSLTQEQKFEHMYDOSLOVPYRNSLRKAHIFGIIPTSFQAMMYFSYAGCFRFG 960
Db 901 IENFRTVSLTQEQKFEHMYAQSLQVPPYRNSLRKAHIFGIIPTSFQAMMYFSYAGCFRFG 960
Qy 961 AYLVAHSLMSPEDVLLVFSVAVFGAMAVGVSSPAPDYAKAKVSAAHIMIIETKPLIDS 1020
Db 961 AYLVAHSLMSPEDVLLVFSVAVFGAMAVGVSSPAPDYAKAKVSAAHIMIIETKPLIDS 1020
Qy 1021 YSTGLKENTLEGNTVFNEVFNYPTRDIPVLQGLSLFVKKGQTLALVSGSGCKSTVV 1080
Db 1021 YSTGLKENTLEGNTVFNEVFNYPTRDIPVLQGLSLFVKKGQTLALVSGSGCKSTVV 1080
Qy 1081 QLLERFYDPLAGVLLDQKEIKQLNVQWMLRAHLGIVSQEPILPDCSISENTAYGNSRVV 1140
Db 1081 QLLERFYDPLAGVLLDQKEIKQLNVQWMLRAHLGIVSQEPILPDCSISENTAYGNSRVV 1140
Qy 1141 SOEEIVRAAKEANIHAFTESLPNKYSTKVGDGTLQSGQKORIAIARALVRQPHILLD 1200
Db 1141 SOEEIVRAAKEANIHAFTESLPNKYSTKVGDGTLQSGQKORIAIARALVRQPHILLD 1200
Qy 1201 EATSALDTESEKVVQEQALDKAREGRTCVIAHRLSTIQNADLIVVFQNGRVEKHEGTHOOL 1260
Db 1201 EATSALDTESEKVVQEQALDKAREGRTCVIAHRLSTIQNADLIVVFQNGRVEKHEGTHOOL 1260
Qy 1261 LAQKGIYFSMVSQAGAKRQ 1280
Db 1261 LAQKGIYFSMVSQAGAKRQ 1280

RESULT 14
5206352-4
; Patent No. 5206352
; APPLICANT: Roninson, Igor B.; Pastan Ira H.; Gottesman, Michael M.
; TITLE OF INVENTION: COMPOSITIONS FOR CLONES CONTAINING DNA
; SEQUENCES ASSOCIATED WITH MULTIDRUG RESISTANCE IN HUMAN CELLS
; NUMBER OF SEQUENCES: 4
; CURRENT APPLICATION DATA:
; FILING DATE: 24-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 892,575
; FILING DATE: 01-AUG-1986
; APPLICATION NUMBER: 845,610
; FILING DATE: 28-MAR-1986
; SEQ ID NO: 4:
; LENGTH: 1280
5206352-4
Query Match 96.6%; Score 6206; DB 7; Length 1280;
Best Local Similarity 96.5%; Pred. No. 0;
Matches 1235; Conservative 20; Mismatches 25; Indels 0; Gaps 0;
Qy 1 MDLEGRNGAGKONFFKLNKSKDKGKPKTVSVFSMFRYSNWLKLYVMVGTLLAII 60
Db 1 MDLEGRNGAGKONFFKLNKSKDKGKPKTVSVFSMFRYSNWLKLYVMVGTLLAII 60
Qy 61 HGAGLPLMMLVFQDMTDTTANAGNLGDLGALLTNSNITDTVPVNMLEDMTYATYISG 120
Db 61 HGAGLPLMMLVFQDMTDTTANAGNLGDLGALLTNSNITDTVPVNMLEDMTYATYISG 120
Qy 121 IGAGVLVAAYIQVSPFCLAGGQIHKTQKQFHAIIMRQEIQWFDVHVGELNTRLTDDVS 180
Db 121 IGAGVLVAAYIQVSPFCLAGGQIHKTQKQFHAIIMRQEIQWFDVHVGELNTRLTDDVS 180
Qy 181 KNEGIGDKIGMPFQSMATFFTGFIVGFTGRGWLTLVLAISPVLGLSAAVWAKILSSFT 240
Db 181 KNEGIGDKIGMPFQSMATFFTGFIVGFTGRGWLTLVLAISPVLGLSAAVWAKILSSFT 240
Qy 241 DXELLAYAKAGVAEVLAAIRTVIAFGQKKELERYNNKLEAKRIGIKKAITANISIG 300

Db 241 DXELLAYAKAGVAEVLAAIRTVIAFGQKKELERYNNKLEAKRIGIKKAITANISIG 300
Qy 301 AAFLLIYASALAFWYGTTLVLVSKEYSIGQVLTVFVSVLIGAFSVGOASPSIEAFANARG 360
Db 301 AAFLLIYASALAFWYGTTLVLVSKEYSIGQVLTVFVSVLIGAFSVGOASPSIEAFANARG 360
Qy 361 AAFEIFIKIIDNKPSIDSYSKSHKPDNIKGNLFNRNVHFSYPSRKEVKILKGLNLKVQSG 420
Db 361 AAFEIFIKIIDNKPSIDSYSKSHKPDNIKGNLFNRNVHFSYPSRKEVKILKGLNLKVQSG 420
Qy 421 QTVALVNSCGSGSTTVLMQRLYDPTGEMVSDGDIRTINVRFLREIIGVVSQEPVLF 480
Db 421 QTVALVNSCGSGSTTVLMQRLYDPTGEMVSDGDIRTINVRFLREIIGVVSQEPVLF 480
Qy 481 ATTIAENIRYGREVDVTMDEIEKAVKANAYDFIMKLPQKPDITLVGERGALSGGOKORIA 540
Db 481 ATTIAENIRYGREVDVTMDEIEKAVKANAYDFIMKLPQKPDITLVGERGALSGGOKORIA 540
Qy 541 IARALVRNPKILLIDENATSDALDTESEAVVOALDKARKGRTTIVIAHRLSTVRNADVIAG 600
Db 541 IARALVRNPKILLIDENATSDALDTESEAVVOALDKARKGRTTIVIAHRLSTVRNADVIAG 600
Qy 601 FDDGVIVKGNHDELMKEKGIYFKLVTMQTAGNEIELENAADESKSIDTLEMSHSDSGS 660
Db 601 FDDGVIVKGNHDELMKEKGIYFKLVTMQTAGNEIELENAADESKSIDTLEMSHSDSGS 660
Qy 661 SLIRKSTRSVRSGSQDRKLSKTEALDESIPPVSFWRMKLNLTWPPVGVVPCALII 720
Db 661 SLIRKSTRSVRSGSQDRKLSKTEALDESIPPVSFWRMKLNLTWPPVGVVPCALII 720
Qy 721 NGGLQPAFNVIFSKIIGIPTNRDDAETKRONSNLFSLLFLVLGIVSFTTLPQFTFGKA 780
Db 721 NGGLQPAFNVIFSKIIGIPTNRDDAETKRONSNLFSLLFLVLGIVSFTTLPQFTFGKA 780
Qy 781 GEILTKELRYMVFRLSRQVSWPDDPKNTTGALTTLANDAAQVKAIGSLRLAITONI 840
Db 781 GEILTKELRYMVFRLSRQVSWPDDPKNTTGALTTLANDAAQVKAIGSLRLAITONI 840
Qy 841 ANLGTGIIISPIYCHQTLTLLLAIVPIIATAGVVMKLSGQALXDKKELEGAGKIATEA 900
Db 841 ANLGTGIIISPIYCHQTLTLLLAIVPIIATAGVVMKLSGQALXDKKELEGAGKIATEA 900
Qy 901 IENFRTVSLTQEQKFEHMYDOSLOVPYRNSLRKAHIFGIIPTSFQAMMYFSYAGCFRFG 960
Db 901 IENFRTVSLTQEQKFEHMYAQSLQVPPYRNSLRKAHIFGIIPTSFQAMMYFSYAGCFRFG 960
Qy 961 AYLVAHSLMSPEDVLLVFSVAVFGAMAVGVSSPAPDYAKAKVSAAHIMIIETKPLIDS 1020
Db 961 AYLVAHSLMSPEDVLLVFSVAVFGAMAVGVSSPAPDYAKAKVSAAHIMIIETKPLIDS 1020
Qy 1021 YSTGLKENTLEGNTVFNEVFNYPTRDIPVLQGLSLFVKKGQTLALVSGSGCKSTVV 1080
Db 1021 YSTGLKENTLEGNTVFNEVFNYPTRDIPVLQGLSLFVKKGQTLALVSGSGCKSTVV 1080
Qy 1081 QLLERFYDPLAGVLLDQKEIKQLNVQWMLRAHLGIVSQEPILPDCSISENTAYGNSRVV 1140
Db 1081 QLLERFYDPLAGVLLDQKEIKQLNVQWMLRAHLGIVSQEPILPDCSISENTAYGNSRVV 1140
Qy 1141 SOEEIVRAAKEANIHAFTESLPNKYSTKVGDGTLQSGQKORIAIARALVRQPHILLD 1200
Db 1141 SOEEIVRAAKEANIHAFTESLPNKYSTKVGDGTLQSGQKORIAIARALVRQPHILLD 1200
Qy 1201 EATSALDTESEKVVQEQALDKAREGRTCVIAHRLSTIQNADLIVVFQNGRVEKHEGTHOOL 1260
Db 1201 EATSALDTESEKVVQEQALDKAREGRTCVIAHRLSTIQNADLIVVFQNGRVEKHEGTHOOL 1260
Qy 1261 LAQKGIYFSMVSQAGAKRQ 1280
Db 1261 LAQKGIYFSMVSQAGAKRQ 1280

QY 1 MDLEGRNGAEGKKNFFKLNKSKDKKPKPTVSFPMFYSNWLKLYVVGTLAAII 60
DB 1 MDLEGRNGAEGKKNFFKLNKSKDKKPKPTVSFPMFYSNWLKLYVVGTLAAII 60
QY 61 HGAGLPLMLVFGDMTDTFANAGLGLDGLALL---TNSNITDTPVPMNLEEDMTRVAY 117
DB 61 HGAGLPLMLVFGDMTDTFANAGLGLDGLALLFNNNTSSNITDTPVPMNLEEDMTRVAY 120
QY 118 YSGIGAGVLAAYIOWSFVCLAAAGROTHKIRKQFPHALMRQEIOWFVHDVDELNTRLT 177
DB 121 YSGIGAGVLAAYIOWSFVCLAAAGROTHKIRKQFPHALMRQEIOWFVHDVDELNTRLT 180
QY 178 DVSKINEGIGDKIMGFQSMATFTFTGIVGTRGWKLTLLVLAISPVGLSAAVWAKILS 237
DB 181 DVSKINEGIGDKIMGFQSMATFTFTGIVGTRGWKLTLLVLAISPVGLSAAVWAKILS 240
QY 238 SPTDKELLAYAKAGAVAEVLAARTVIAFGGQKKELERYNKNLEAKRIGIKKAITANI 297
DB 241 SPTDKELLAYAKAGAVAEVLAARTVIAFGGQKKELERYNKNLEAKRIGIKKAITANI 300
QY 298 SIGAFLIIVASYALAFWYGTTLVLSKEYSISGOVLTVPFVSVLIGAFSVOGASPSIEAPAN 357
DB 301 SIGAFLIIVASYALAFWYGTTLVLSKEYSISGOVLTVPFVSVLIGAFSVOGASPSIEAPAN 360
QY 358 ARGAAFEIFKIIDNKPSIDSYSGSKGHPDNIKGNLEFRNVHFSYPSRKEVKILKGLNLKV 417
DB 361 ARGAAFEIFKIIDNKPSIDSYSGSKGHPDNIKGNLEFRNVHFSYPSRKEVKILKGLNLKV 420
QY 418 QSGQTVLVGNSGCKSTTVQLMORLVDPTGMSVVDGODTIRTNVPLREIIGVVSQEP 477
DB 421 QSGQTVLVGNSGCKSTTVQLMORLVDPTGMSVVDGODTIRTNVPLREIIGVVSQEP 480
QY 478 VLFATTAEINRYGREDVTMDIEIKAVKEAANAYDFIMKLPOKFTDLVGERGAQLSGGQK 537
DB 481 VLFATTAEINRYGREDVTMDIEIKAVKEAANAYDFIMKLPOKFTDLVGERGAQLSGGQK 540
QY 538 RIAIARALVRNPKILLDEATSAIDTSEAVVQVALDKARKGRTTIVIAHRLSTVRNADV 597
DB 541 RIAIARALVRNPKILLDEATSAIDTSEAVVQVALDKARKGRTTIVIAHRLSTVRNADV 600
QY 598 IAGFDGIVVKGNDHLMKSGIYFKLVMTQAGNEIELENADESKSEIDTLEMSSHD 657
DB 601 IAGFDGIVVKGNDHLMKSGIYFKLVMTQAGNEIELENADESKSEIDTLEMSSHD 660
QY 658 SGSSILRKSTRSRVSGQGDRLSTKEALDESIPVPSFWIRIMKLNLTENPFYVGVGFC 717
DB 661 SGSSILRKSTRSRVSGQGDRLSTKEALDESIPVPSFWIRIMKLNLTENPFYVGVGFC 720
QY 718 AINGGLQPAFAVIFSKIIGIFTRNDDAETKQNSNLSLLFLVLGIVSFTFFLQGTFF 777
DB 721 AINGGLQPAFAVIFSKIIGIFTRNDDAETKQNSNLSLLFLVLGIVSFTFFLQGTFF 780
QY 778 GKAGEILTKRLRYVWFRSMLQDVSFDDPKNTTGALTTRLANDAAOVKGAIGSLAII 837
DB 781 GKAGEILTKRLRYVWFRSMLQDVSFDDPKNTTGALTTRLANDAAOVKGAIGSLAII 840
QY 838 QNIANLGTGIIISLYGHQTLTLLAIVIPITAIAGVEMKMLSGQALKDKELEGAGKIA 897
DB 841 QNIANLGTGIIISLYGHQTLTLLAIVIPITAIAGVEMKMLSGQALKDKELEGAGKIA 900
QY 898 TEAIENFRVSLTQEQFEMHYDQSLQVPRNSLRKAHIFGITSFTQAMMYFSYACGF 957
DB 901 TEAIENFRVSLTQEQFEMHYDQSLQVPRNSLRKAHIFGITSFTQAMMYFSYACGF 960
QY 958 RFYAYLVASHLSMDFEDVLLVSFVAVGAWVGVSSFAPDYAKAVSAHHIIMIEKTP 1017
DB 961 RFYAYLVASHLSMDFEDVLLVSFVAVGAWVGVSSFAPDYAKAVSAHHIIMIEKTP 1020
QY 1018 IDSYSYEGKPNLTGENTFNEVFNYPTRLDIPVLQGLSLVKKGTALVGSSSGCKS 1077
DB 1021 IDSYSYEGKPNLTGENTFNEVFNYPTRLDIPVLQGLSLVKKGTALVGSSSGCKS 1080
QY 1078 TVVQLLERYDPLAGKVLDDGKEIKQLNVQWRAHLGIVSQBPILFDCSISENIAIGDNS 1137

DB 1081 TVVQLLERYDPLAGKVLDDGKEIKQLNVQWRAHLGIVSQBPILFDCSISENIAIGDNS 1140
QY 1138 RVVSQBEIVRAAKEANIHFIESLNPKNKYSTRVGDGKQTLGGQKQRIARALVROPHIL 1197
DB 1141 RVVSQBEIVRAAKEANIHFIESLNPKNKYSTRVGDGKQTLGGQKQRIARALVROPHIL 1200
QY 1198 LDEATSAIDTSEKVVQALDKARGRCTIVIAHRLSTIONADLIVFQNGRVKRGHGT 1257
DB 1201 LDEATSAIDTSEKVVQALDKARGRCTIVIAHRLSTIONADLIVFQNGRVKRGHGT 1260
QY 1258 QQLLAOKGIYFMSVSVQAGAKRQ 1280
DB 1261 QQLLAOKGIYFMSVSVQAGAKRQ 1283

RESULT 6

US-09-584-586-2
Sequence 2, Application US/09584586
Feature No. 633-350

GENERAL INFORMATION:

APPLICANT: Sorrentino, Brian
TITLE OF INVENTION: EXPANSION OF HEMATOPOIETIC STEM CELLS TRANSDUCED WITH
TITLE OF INVENTION: MDR-1 METHODS OF USE THEREOF
FILE REFERENCES: 1340-1-021CIP
CURRENT APPLICATION NUMBER: US/09/584,586
CURRENT FILING DATE: 2000-05-31
EARLIER APPLICATION NUMBER: US 60/086,988
EARLIER FILING DATE: 1998-05-28
EARLIER APPLICATION NUMBER: PCT/US99/11825
EARLIER FILING DATE: 1999-05-27
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 1280
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Human MDR 185-G
US-09-584-586-2

Query Match 96.8%; Score 6218; DB 2; Length 1280;
Best Local Similarity 96.6%; Pred. No. 0;
Matches 123; Conservative 19; Mismatches 24; Indels 0; Gaps 0;

QY 1 MDLEGRNGAEGKKNFFKLNKSKDKKPKPTVSFPMFYSNWLKLYVVGTLAAII 60
DB 1 MDLEGRNGAEGKKNFFKLNKSKDKKPKPTVSFPMFYSNWLKLYVVGTLAAII 60
QY 61 HGAGLPLMLVFGDMTDTFANAGLGLDGLALLTNSNITDTPVPMNLEEDMTRVAYYSG 120
DB 61 HGAGLPLMLVFGDMTDTFANAGLGLDGLALLTNSNITDTPVPMNLEEDMTRVAYYSG 120
QY 121 IGAGLVAAIYQVSWFVCLAAAGROTHKIRKQFPHALMRQEIOWFVHDVDELNTRLTDDVS 180
DB 121 IGAGLVAAIYQVSWFVCLAAAGROTHKIRKQFPHALMRQEIOWFVHDVDELNTRLTDDVS 180
QY 181 KINEGIGDKIMGFQSMATFTFTGIVGTRGWKLTLLVLAISPVGLSAAVWAKILSFT 240
DB 181 KINEGIGDKIMGFQSMATFTFTGIVGTRGWKLTLLVLAISPVGLSAAVWAKILSFT 240
QY 241 DKELLAYAKAGAVAEVLAARTVIAFGGQKKELERYNKNLEAKRIGIKKAITANISIG 300
DB 241 DKELLAYAKAGAVAEVLAARTVIAFGGQKKELERYNKNLEAKRIGIKKAITANISIG 300
QY 301 AAFLLIIVASYALAFWYGTTLVLSKEYSISGOVLTVPFVSVLIGAFSVOGASPSIEAFANAR 360
DB 301 AAFLLIIVASYALAFWYGTTLVLSKEYSISGOVLTVPFVSVLIGAFSVOGASPSIEAFANAR 360
QY 361 AAFIFKIIDNKPSIDSYSGSKGHPDNIKGNLEFRNVHFSYPSRKEVKILKGLNLKVQSG 420
DB 361 AAFIFKIIDNKPSIDSYSGSKGHPDNIKGNLEFRNVHFSYPSRKEVKILKGLNLKVQSG 420


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; FILE REFERENCE: 015280-402100US
; CURRENT APPLICATION NUMBER: US/09/767,594
; CURRENT FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: US 60/177,410
; PRIOR FILING DATE: 2000-01-20
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1280
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human P-glycoprotein (Pgp)/multi-drug resistance 1
; OTHER INFORMATION: (Mdr-1) ATP-binding cassette (ABC transporter)
; OTHER INFORMATION: protein
; US-09-767-594-2

Query Match      96.6%; Score 6209; DB 2; Length 1280;
Best Local Similarity 96.6%; Pred. No. 0;
Matches 1236; Conservative 19; Mismatches 25; Indels 0; Gaps 0;

QY 121 OTVALVNSGCGKSTTVQLMORLYDPTGVMVSDGDIRTNVRFLEIIGVVSQEPVLF 480
DB 121 OTVALVNSGCGKSTTVQLMORLYDPTGVMVSDGDIRTNVRFLEIIGVVSQEPVLF 480
QY 481 ATTIAENIRYGRDVTMDIEKAVKEANAYDFIMKLPKEDTLVGERGAQLSGQKORIA 540
DB 481 ATTIAENIRYGRDVTMDIEKAVKEANAYDFIMKLPKEDTLVGERGAQLSGQKORIA 540
QY 541 IARALVRNPKILLDEATSAIDTSEAVVQVALDKARKGRTTIVIAHRLSTVRNADVIAG 600
DB 541 IARALVRNPKILLDEATSAIDTSEAVVQVALDKARKGRTTIVIAHRLSTVRNADVIAG 600
QY 601 FDDGVIVEKGNHDELMEKEGIYFKLVTMTAGNEIELENAADESKSIDTLEMSHSDSGS 660
DB 601 FDDGVIVEKGNHDELMEKEGIYFKLVTMTAGNEIELENAADESKSIDTLEMSHSDSGS 660
QY 661 SLIRKSTRSVRGSGQDRKLSLTKALDESIPVPSFWRIMKLNLTWEPYFVGVFCAII 720
DB 661 SLIRKSTRSVRGSGQDRKLSLTKALDESIPVPSFWRIMKLNLTWEPYFVGVFCAII 720
QY 721 NGGLQAPAFVIFSKIIIGFTNDDAETKRONSNLPSLLFLVLGTVSPITTEFLOGFTFGKA 780
DB 721 NGGLQAPAFVIFSKIIIGFTNDDAETKRONSNLPSLLFLVLGTVSPITTEFLOGFTFGKA 780
QY 781 GEILTKELRYWFRSMLRQDVSWFDDPKNTTGALTTRLANDAAQVKAIGSRLAIIITQNI 840
DB 781 GEILTKELRYWFRSMLRQDVSWFDDPKNTTGALTTRLANDAAQVKAIGSRLAIIITQNI 840
QY 841 ANLGTGIIISIIYGVQWLTLLLAIVPIIAIAGVVMKLSGOALKDKKELEGAGKIATEA 900
DB 841 ANLGTGIIISIIYGVQWLTLLLAIVPIIAIAGVVMKLSGOALKDKKELEGAGKIATEA 900
QY 901 IENFRVTVSLTOEQKPEHMAQSLQVPRNSLRKAHIFGTFESPTQAMTFFSVAGCFRFG 960
DB 901 IENFRVTVSLTOEQKPEHMAQSLQVPRNSLRKAHIFGTFESPTQAMTFFSVAGCFRFG 960
QY 961 AYLVAHSLMSPEDVLLVFSVAVFGAMAVGVSSFAPDYAKAKVSAAHIMIEKTPILDS 1020
DB 961 AYLVAHSLMSPEDVLLVFSVAVFGAMAVGVSSFAPDYAKAKVSAAHIMIEKTPILDS 1020
QY 1021 YSTEGLKNTLEGNVTNEVFNYPTRLDIPVLOGLSLEVKKGQTLVAGSSGCGKSTTV 1080
DB 1021 YSTEGLKNTLEGNVTNEVFNYPTRLDIPVLOGLSLEVKKGQTLVAGSSGCGKSTTV 1080
QY 1081 QLLERFYDPLAGKVLDDKETKOLNVOLRAHLGIVSQEPIFLPCSIENIAYGDSRVV 1140
DB 1081 QLLERFYDPLAGKVLDDKETKOLNVOLRAHLGIVSQEPIFLPCSIENIAYGDSRVV 1140
QY 1141 SQEIVRAAKEANTHAFIESLPNKYSTRVGDKGTQLSGQKORIAIARALVRPHILLD 1200
DB 1141 SQEIVRAAKEANTHAFIESLPNKYSTRVGDKGTQLSGQKORIAIARALVRPHILLD 1200
QY 1201 EATSALDTESEKVOEALDKAREGTCIVIAHRLSTTONADLIVVFONGRVKHEGTHQOL 1260
DB 1201 EATSALDTESEKVOEALDKAREGTCIVIAHRLSTTONADLIVVFONGRVKHEGTHQOL 1260
QY 1261 LAQKGIYFSMVSVQAGAKRQ 1280
DB 1261 LAQKGIYFSMVSVQAGAKRQ 1280

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; FILE REFERENCE: 015280-402100US
; CURRENT APPLICATION NUMBER: US/09/767,594
; CURRENT FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: US 60/177,410
; PRIOR FILING DATE: 2000-01-20
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1280
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human P-glycoprotein (Pgp)/multi-drug resistance 1
; OTHER INFORMATION: (Mdr-1) ATP-binding cassette (ABC transporter)
; OTHER INFORMATION: protein
; US-09-767-594-2

Query Match      96.6%; Score 6209; DB 2; Length 1280;
Best Local Similarity 96.6%; Pred. No. 0;
Matches 1236; Conservative 19; Mismatches 25; Indels 0; Gaps 0;

QY 121 OTVALVNSGCGKSTTVQLMORLYDPTGVMVSDGDIRTNVRFLEIIGVVSQEPVLF 480
DB 121 OTVALVNSGCGKSTTVQLMORLYDPTGVMVSDGDIRTNVRFLEIIGVVSQEPVLF 480
QY 481 ATTIAENIRYGRDVTMDIEKAVKEANAYDFIMKLPKEDTLVGERGAQLSGQKORIA 540
DB 481 ATTIAENIRYGRDVTMDIEKAVKEANAYDFIMKLPKEDTLVGERGAQLSGQKORIA 540
QY 541 IARALVRNPKILLDEATSAIDTSEAVVQVALDKARKGRTTIVIAHRLSTVRNADVIAG 600
DB 541 IARALVRNPKILLDEATSAIDTSEAVVQVALDKARKGRTTIVIAHRLSTVRNADVIAG 600
QY 601 FDDGVIVEKGNHDELMEKEGIYFKLVTMTAGNEIELENAADESKSIDTLEMSHSDSGS 660
DB 601 FDDGVIVEKGNHDELMEKEGIYFKLVTMTAGNEIELENAADESKSIDTLEMSHSDSGS 660
QY 661 SLIRKSTRSVRGSGQDRKLSLTKALDESIPVPSFWRIMKLNLTWEPYFVGVFCAII 720
DB 661 SLIRKSTRSVRGSGQDRKLSLTKALDESIPVPSFWRIMKLNLTWEPYFVGVFCAII 720
QY 721 NGGLQAPAFVIFSKIIIGFTNDDAETKRONSNLPSLLFLVLGTVSPITTEFLOGFTFGKA 780
DB 721 NGGLQAPAFVIFSKIIIGFTNDDAETKRONSNLPSLLFLVLGTVSPITTEFLOGFTFGKA 780

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; FILE REFERENCE: 015280-402100US
; CURRENT APPLICATION NUMBER: US/09/767,594
; CURRENT FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: US 60/177,410
; PRIOR FILING DATE: 2000-01-20
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1280
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human P-glycoprotein (Pgp)/multi-drug resistance 1
; OTHER INFORMATION: (Mdr-1) ATP-binding cassette (ABC transporter)
; OTHER INFORMATION: protein
; US-09-767-594-2

Query Match      96.6%; Score 6209; DB 2; Length 1280;
Best Local Similarity 96.6%; Pred. No. 0;
Matches 1236; Conservative 19; Mismatches 25; Indels 0; Gaps 0;

QY 121 OTVALVNSGCGKSTTVQLMORLYDPTGVMVSDGDIRTNVRFLEIIGVVSQEPVLF 480
DB 121 OTVALVNSGCGKSTTVQLMORLYDPTGVMVSDGDIRTNVRFLEIIGVVSQEPVLF 480
QY 481 ATTIAENIRYGRDVTMDIEKAVKEANAYDFIMKLPKEDTLVGERGAQLSGQKORIA 540
DB 481 ATTIAENIRYGRDVTMDIEKAVKEANAYDFIMKLPKEDTLVGERGAQLSGQKORIA 540
QY 541 IARALVRNPKILLDEATSAIDTSEAVVQVALDKARKGRTTIVIAHRLSTVRNADVIAG 600
DB 541 IARALVRNPKILLDEATSAIDTSEAVVQVALDKARKGRTTIVIAHRLSTVRNADVIAG 600
QY 601 FDDGVIVEKGNHDELMEKEGIYFKLVTMTAGNEIELENAADESKSIDTLEMSHSDSGS 660
DB 601 FDDGVIVEKGNHDELMEKEGIYFKLVTMTAGNEIELENAADESKSIDTLEMSHSDSGS 660
QY 661 SLIRKSTRSVRGSGQDRKLSLTKALDESIPVPSFWRIMKLNLTWEPYFVGVFCAII 720
DB 661 SLIRKSTRSVRGSGQDRKLSLTKALDESIPVPSFWRIMKLNLTWEPYFVGVFCAII 720
QY 721 NGGLQAPAFVIFSKIIIGFTNDDAETKRONSNLPSLLFLVLGTVSPITTEFLOGFTFGKA 780
DB 721 NGGLQAPAFVIFSKIIIGFTNDDAETKRONSNLPSLLFLVLGTVSPITTEFLOGFTFGKA 780

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RESULT 7
US-09-767-594-2
Sequence 2, Application US/09767594
Patent No. 6521635
GENERAL INFORMATION:
APPLICANT: Bates, Susan
APPLICANT: Robey, Robert
APPLICANT: The Government of the United States of America
APPLICANT: as represented by the Secretary of the
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Inhibition of MDR Transport by Acridine Derivatives

QY 1141 SOEIVRAAKEANIHAFIESLPNKYSTKVGDKGTOLSGGQKORIAARALVRPHILLD 1200
 DB 1141 SOEIVRAAKEANIHAFIESLPNKYSTKVGDKGTOLSGGQKORIAARALVRPHILLD 1200
 QY 1201 EATSALDTESEKVVQVQALDKAREGTCIVIAHRLSTIQNADLIIVVFQNGRVEKHGTHQOL 1260
 DB 1201 EATSALDTESEKVVQVQALDKAREGTCIVIAHRLSTIQNADLIIVVFQNGRVEKHGTHQOL 1260
 QY 1261 LAQKGIYFMSVMSVQAGTKRQ 1280
 DB 1261 LAQKGIYFMSVMSVQAGTKRQ 1280

RESULT 4

US-10-101-433A-5

; Sequence 5, Application US/10101433A

; Patent No. 6855812

; GENERAL INFORMATION:

; APPLICANT: Hanscom, Sara

; APPLICANT: Crespi, Charles

; TITLE OF INVENTION: P-GLYCOPROTEINS AND USES THEREOF

; FILE REFERENCE: G00307/70019

; CURRENT APPLICATION NUMBER: US/10/101,433A

; CURRENT FILING DATE: 2002-03-19

; PRIOR APPLICATION NUMBER: US 60/277,095

; PRIOR FILING DATE: 2001-03-19

; NUMBER OF SEQ ID NOS: 38

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 5

; LENGTH: 1280

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-101-433A-5

Query Match 100.0%; Score 6431; DB 2; Length 1280;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDLEGRNGGAKKGNFFFLANKSKKCKKPTVSFSPRYSNWLDKLYWVGTLAAII 60
 DB 1 MDLEGRNGGAKKGNFFFLANKSKKCKKPTVSFSPRYSNWLDKLYWVGTLAAII 60
 QY 61 HGAGLPLMLVFGEMTDIPANAGNLEDMSNITNRSNDINDTGFPMNLEEDMTYAYYS 120
 DB 61 HGAGLPLMLVFGEMTDIPANAGNLEDMSNITNRSNDINDTGFPMNLEEDMTYAYYS 120
 QY 121 IGAGVLVAAYIOVSFWCLAGROIHKIRKOPFHAIINROEIGWPDVHDVGEINRLTDDVS 180
 DB 121 IGAGVLVAAYIOVSFWCLAGROIHKIRKOPFHAIINROEIGWPDVHDVGEINRLTDDVS 180
 QY 181 KINEVIGDKIGMFFQSMATFFTGFIIVGTRGWKLTVLILAIISPLVGLSAVWAKILSSPT 240
 DB 181 KINEVIGDKIGMFFQSMATFFTGFIIVGTRGWKLTVLILAIISPLVGLSAVWAKILSSPT 240
 QY 241 DKELLAYAKAGAAVEVLAAITVIAFGQCKELERYNNKLEAKRIGIKKAITANISIG 300
 DB 241 DKELLAYAKAGAAVEVLAAITVIAFGQCKELERYNNKLEAKRIGIKKAITANISIG 300
 QY 301 AAFLLIYASYALAFWGTTLVLSGEYSIGOVLTVPFVSVLIGAFSGVQASPSPEAFANARG 360
 DB 301 AAFLLIYASYALAFWGTTLVLSGEYSIGOVLTVPFVSVLIGAFSGVQASPSPEAFANARG 360
 QY 361 AAYEIFIKIDNKPISDYSKSGHKPDNKNLEFRNVHFSYPSRKEVKILKGLNKVQSG 420
 DB 361 AAYEIFIKIDNKPISDYSKSGHKPDNKNLEFRNVHFSYPSRKEVKILKGLNKVQSG 420
 QY 421 QTVALVNSGCGKSTTVLMQRLDPTDTEGMVSVVDQDRTINVRFLREIIGWSEPVLF 480
 DB 421 QTVALVNSGCGKSTTVLMQRLDPTDTEGMVSVVDQDRTINVRFLREIIGWSEPVLF 480
 QY 481 ATTIAENIRYGRNVMTDEIEKAVKEANAYDFIMKLPKPDTLVGERGAOLSGGQKORIA 540

DB 481 ATTIAENIRYGRNVMTDEIEKAVKEANAYDFIMKLPKPDTLVGERGAOLSGGQKORIA 540
 QY 541 IARALVRNPKILLDDATSAALDTESEKVVQVQALDKAREGTCIVIAHRLSTIQNADLIIVVFQNGRVEKHGTHQOL 600
 DB 541 IARALVRNPKILLDDATSAALDTESEKVVQVQALDKAREGTCIVIAHRLSTIQNADLIIVVFQNGRVEKHGTHQOL 600
 QY 601 FDDGVIVEKGNHDELMKEKGIYFKLVMTOTAGNEVELENADESKSEIDALEMSNDSSRS 660
 DB 601 FDDGVIVEKGNHDELMKEKGIYFKLVMTOTAGNEVELENADESKSEIDALEMSNDSSRS 660
 QY 661 SLIRKSTRRSVRGSOAQRKLSKEALDESIPVSWRIMKLNITWPFYVGVFCALI 720
 DB 661 SLIRKSTRRSVRGSOAQRKLSKEALDESIPVSWRIMKLNITWPFYVGVFCALI 720
 QY 721 NGGLOPAPALIFSKIIIGVFTTRIDDPETKRONSLFSLFLAIGIISFTTFFLQGTFFOKA 780
 DB 721 NGGLOPAPALIFSKIIIGVFTTRIDDPETKRONSLFSLFLAIGIISFTTFFLQGTFFOKA 780
 QY 781 GEILTKRLRYMFRSMLRQDVSWFDDPKNTTGALTTRLANDAAOVKGAIGSRLAVITONI 840
 DB 781 GEILTKRLRYMFRSMLRQDVSWFDDPKNTTGALTTRLANDAAOVKGAIGSRLAVITONI 840
 QY 841 ANLCTGIIISFIYQWLTLLLAIVPIIAIAGVVEMLSGOALKKKELEGAGKIATEA 900
 DB 841 ANLCTGIIISFIYQWLTLLLAIVPIIAIAGVVEMLSGOALKKKELEGAGKIATEA 900
 QY 901 IENFRTVVSLTQEQPEHMAQSLQVFPYNSLRKAHIFGITFTFTQMTWYFVAGCFRFG 960
 DB 901 IENFRTVVSLTQEQPEHMAQSLQVFPYNSLRKAHIFGITFTFTQMTWYFVAGCFRFG 960
 QY 961 AYLVAHKLMSFEDVLLVFSVAVFGMAVGVQVSPFADYAKAKISAAHIMIIEKTPILDS 1020
 DB 961 AYLVAHKLMSFEDVLLVFSVAVFGMAVGVQVSPFADYAKAKISAAHIMIIEKTPILDS 1020
 QY 1021 YSTEGMLPNTLEGNTVTFGEVWYNYPRDIPVLQGLSLEVKGQTLALVSSGCGKSTV 1080
 DB 1021 YSTEGMLPNTLEGNTVTFGEVWYNYPRDIPVLQGLSLEVKGQTLALVSSGCGKSTV 1080
 QY 1081 QLLERFYDPLAGKVLIDGKEIKRLNVQWLRHGLGVSOEPIFLDCSIAENIAYGNSRV 1140
 DB 1081 QLLERFYDPLAGKVLIDGKEIKRLNVQWLRHGLGVSOEPIFLDCSIAENIAYGNSRV 1140
 QY 1141 SOEIVRAAKEANIHAFIESLPNKYSTKVGDKGTOLSGGQKORIAARALVRPHILLD 1200
 DB 1141 SOEIVRAAKEANIHAFIESLPNKYSTKVGDKGTOLSGGQKORIAARALVRPHILLD 1200
 QY 1201 EATSALDTESEKVVQVQALDKAREGTCIVIAHRLSTIQNADLIIVVFQNGRVEKHGTHQOL 1260
 DB 1201 EATSALDTESEKVVQVQALDKAREGTCIVIAHRLSTIQNADLIIVVFQNGRVEKHGTHQOL 1260
 QY 1261 LAQKGIYFMSVMSVQAGTKRQ 1280
 DB 1261 LAQKGIYFMSVMSVQAGTKRQ 1280

RESULT 5

US-09-817-762-3

; Sequence 3, Application US/09817762

; Patent No. 6858774

; GENERAL INFORMATION:

; APPLICANT: Spalding, Edgar P.

; APPLICANT: No. 6858774, Bost

; TITLE OF INVENTION: MDR-Like ABC Transporter Gene From

; TITLE OF INVENTION: Plants

; FILE REFERENCE: 13238-00061

; CURRENT APPLICATION NUMBER: US/09/817,762

; CURRENT FILING DATE: 2001-03-26

; PRIOR APPLICATION NUMBER: PCT/US99/22363

; PRIOR FILING DATE: 1999-09-24

; PRIOR APPLICATION NUMBER: US 60/101,814

; PRIOR FILING DATE: 1998-09-25

; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: FastSeq for Windows Version 4.0

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; SEQ ID NO 3
; LENGTH: 1280
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Genbank P08183
; DATABASE ENTRY DATE: 1997-11-01
US-09-817-762-3

Query Match      100.0%; Score 6431; DB 2; Length 1280;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDLEGRNGAKKQKFFKLNKSEKDKKPKPTVSFMSFRYSNMLDKLYMVVGTAAII 60
DB 1 MDLEGRNGAKKQKFFKLNKSEKDKKPKPTVSFMSFRYSNMLDKLYMVVGTAAII 60
QY 61 HGAGLPLMWLVFGEWTDIPANAGNLEDLMSNITNRSNDINDTGFNNLEEDMTRYAYISG 120
DB 61 HGAGLPLMWLVFGEWTDIPANAGNLEDLMSNITNRSNDINDTGFNNLEEDMTRYAYISG 120
QY 121 IGAGVLVAAYIQVSWFCLAAAGQIHKIRKQFFHAIMRQEIQWDFVHDVGLNLTDDVS 180
DB 121 IGAGVLVAAYIQVSWFCLAAAGQIHKIRKQFFHAIMRQEIQWDFVHDVGLNLTDDVS 180
QY 181 KINEVIGDKIMPFQSMATFTTGFIVGTRGWKLTIVLAISPVLGLSAVWAKILSFT 240
DB 181 KINEVIGDKIMPFQSMATFTTGFIVGTRGWKLTIVLAISPVLGLSAVWAKILSFT 240
QY 241 KELLAYAKAGAVAEVLAAITVIAFGGKKELEKRYNKNLEAKRIGIKKAITANISIG 300
DB 241 KELLAYAKAGAVAEVLAAITVIAFGGKKELEKRYNKNLEAKRIGIKKAITANISIG 300
QY 301 RAFLIYASYALAFYGTTLVLSGEYSIGQVLTVPFSLVIGAFSGVQASPSIEAFANRG 360
DB 301 RAFLIYASYALAFYGTTLVLSGEYSIGQVLTVPFSLVIGAFSGVQASPSIEAFANRG 360
QY 361 AAYEIFKIIDNPKSIDSYSGKHGPDNINKNLEFRNVHPSYPSRKEVKILKGLNKVQSG 420
DB 361 AAYEIFKIIDNPKSIDSYSGKHGPDNINKNLEFRNVHPSYPSRKEVKILKGLNKVQSG 420
QY 421 QTVLVGNSGCKSTTVQMLQRLYDTEGMSVSDGQDITINVRFLREIIGVVSQEPVLF 480
DB 421 QTVLVGNSGCKSTTVQMLQRLYDTEGMSVSDGQDITINVRFLREIIGVVSQEPVLF 480
QY 481 ATTIAENIRYGRNVMTDIEKAVKEANAYDFIMKLPHKFDTLVGERGAQLSGGQKRIA 540
DB 481 ATTIAENIRYGRNVMTDIEKAVKEANAYDFIMKLPHKFDTLVGERGAQLSGGQKRIA 540
QY 541 IARALVRNPKILLDEATSALETSSEAVVQVALDKARKGRTTIVIAHRLSTVRNADVIAG 600
DB 541 IARALVRNPKILLDEATSALETSSEAVVQVALDKARKGRTTIVIAHRLSTVRNADVIAG 600
QY 601 PDGVIKGNHDELMEKGIYFKLVMTQTAGNEVELENADESKEIDALESSNDSRS 660
DB 601 PDGVIKGNHDELMEKGIYFKLVMTQTAGNEVELENADESKEIDALESSNDSRS 660
QY 661 SLIRKSTRSRVSGQAQDRKLTKEALDESIPVPSFWMKLNLTWEPYFVGVVFCALII 720
DB 661 SLIRKSTRSRVSGQAQDRKLTKEALDESIPVPSFWMKLNLTWEPYFVGVVFCALII 720
QY 721 NGGLQAPAFIISKIIIGVTRIDDDPETKQNSNLSLLFLALGIIISPIITFLOGTFGKA 780
DB 721 NGGLQAPAFIISKIIIGVTRIDDDPETKQNSNLSLLFLALGIIISPIITFLOGTFGKA 780
QY 781 GBILTKRLRYMYFRSMLRQDWSWFDPKNTTGALTTRLANDAAQVKAIGSLAVITQNI 840
DB 781 GBILTKRLRYMYFRSMLRQDWSWFDPKNTTGALTTRLANDAAQVKAIGSLAVITQNI 840
QY 841 ANLGTGIIISFYGWQLTLLLAIVPIIAIAGVVENKMLSGQALKDQKLEGAGKIATEA 900
DB 841 ANLGTGIIISFYGWQLTLLLAIVPIIAIAGVVENKMLSGQALKDQKLEGAGKIATEA 900

QY 901 IENFTVVSILTQEQKPEHMYAQSLOVPYRNSLRKAHIFGITFSFTQAMMYSYAGCFRFG 960
DB 901 IENFTVVSILTQEQKPEHMYAQSLOVPYRNSLRKAHIFGITFSFTQAMMYSYAGCFRFG 960
QY 961 AYLVAHKLMSPEDVLLVFSVFGAMAVGVSSPAPYAKAKISAHHIIMIEKTPILDS 1020
DB 961 AYLVAHKLMSPEDVLLVFSVFGAMAVGVSSPAPYAKAKISAHHIIMIEKTPILDS 1020
QY 1021 YSTGLMPTNTEGNTVTFGEVVFNPTPRDIPVLOGLSLEVKKGOTLALVSSGCGKSTVV 1080
DB 1021 YSTGLMPTNTEGNTVTFGEVVFNPTPRDIPVLOGLSLEVKKGOTLALVSSGCGKSTVV 1080
QY 1081 QLLSERFYDPLAGKLLDGKEIKRLNVQWLRHLAGLIVSQEPILFDCSIAENIAYGDSRVV 1140
DB 1081 QLLSERFYDPLAGKLLDGKEIKRLNVQWLRHLAGLIVSQEPILFDCSIAENIAYGDSRVV 1140
QY 1141 SOBEIVRAAKEANTHAFIESLPNKYSTKVGDKGTQSGQKQRIARALVRQPHILLD 1200
DB 1141 SOBEIVRAAKEANTHAFIESLPNKYSTKVGDKGTQSGQKQRIARALVRQPHILLD 1200
QY 1201 EATSALDTSEKVVQVQALDKAREGTCIVIAHRLSTIONADLIIVFQNGRVKEHGHQOL 1260
DB 1201 EATSALDTSEKVVQVQALDKAREGTCIVIAHRLSTIONADLIIVFQNGRVKEHGHQOL 1260
QY 1261 LAQKGIYFSMVSVQAGTKRQ 1280
DB 1261 LAQKGIYFSMVSVQAGTKRQ 1280

RESULT 6
US-09-584-586-4
; Sequence 4, Application US/09584586
; Patent No. 6533150
; GENERAL INFORMATION:
; APPLICANT: Sorrentino, Brian
; APPLICANT: Bunting, Kevin
; TITLE OF INVENTION: EXPANSION OF HEMATOPOIETIC STEM CELLS TRANSDUCED WITH
; TITLE OF INVENTION: MDR-1 METHODS OF USE THEREOF
; FILE REFERENCE: 1340-1-021CIP
; CURRENT APPLICATION NUMBER: US/09/584,586
; CURRENT FILING DATE: 2000-05-31
; EARLIER APPLICATION NUMBER: US 60/086,988
; EARLIER FILING DATE: 1998-05-28
; EARLIER APPLICATION NUMBER: PCT/US99/11825
; EARLIER FILING DATE: 1999-05-27
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 4
; LENGTH: 1280
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Human MDR 185-V
US-09-584-586-4

Query Match      100.0%; Score 6431; DB 2; Length 1280;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDLEGRNGAKKQKFFKLNKSEKDKKPKPTVSFMSFRYSNMLDKLYMVVGTAAII 60
DB 1 MDLEGRNGAKKQKFFKLNKSEKDKKPKPTVSFMSFRYSNMLDKLYMVVGTAAII 60
QY 61 HGAGLPLMWLVFGEWTDIPANAGNLEDLMSNITNRSNDINDTGFNNLEEDMTRYAYISG 120
DB 61 HGAGLPLMWLVFGEWTDIPANAGNLEDLMSNITNRSNDINDTGFNNLEEDMTRYAYISG 120
QY 121 IGAGVLVAAYIQVSWFCLAAAGQIHKIRKQFFHAIMRQEIQWDFVHDVGLNLTDDVS 180
DB 121 IGAGVLVAAYIQVSWFCLAAAGQIHKIRKQFFHAIMRQEIQWDFVHDVGLNLTDDVS 180
QY 181 KINEVIGDKIMPFQSMATFTTGFIVGTRGWKLTIVLAISPVLGLSAVWAKILSFT 240
DB 181 KINEVIGDKIMPFQSMATFTTGFIVGTRGWKLTIVLAISPVLGLSAVWAKILSFT 240
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Db 181 KINEVIGDKIGMFFQSMATFTGTGIVGTGKWKTLVLIALSPVLGSAVWAKILSSFT 240
Qy 241 DKELLAYAKAGAVAEVLAARTVIAFGGQKKELRYNKNLEAKRIGIKKAITANISIG 300
Db 241 DKELLAYAKAGAVAEVLAARTVIAFGGQKKELRYNKNLEAKRIGIKKAITANISIG 300
Qy 301 AAFLLIYASALAFWYGTTLVLSEYSGIVLTVPFVSLGAFSGVQASPSIEAFANARG 360
Db 301 AAFLLIYASALAFWYGTTLVLSEYSGIVLTVPFVSLGAFSGVQASPSIEAFANARG 360
Qy 361 AAYEIFIKIDNKPSIDSKSGHKPDNIKGNLEPNVHPSYPSRKYKILKGLNKLKQSG 420
Db 361 AAYEIFIKIDNKPSIDSKSGHKPDNIKGNLEPNVHPSYPSRKYKILKGLNKLKQSG 420
Qy 421 QTVLVGNSGCGKSTTVOLMORLYDPTGEMVSDGQDRTINVRFLREIIGVVSQBPVLF 480
Db 421 QTVLVGNSGCGKSTTVOLMORLYDPTGEMVSDGQDRTINVRFLREIIGVVSQBPVLF 480
Qy 481 ATTIAENIRYGRNVWDETEKAVEANAYDFIMKLPKEDTLVGERGAOLSGGOKORIA 540
Db 481 ATTIAENIRYGRNVWDETEKAVEANAYDFIMKLPKEDTLVGERGAOLSGGOKORIA 540
Qy 541 IARALVENPKILLDEATSDALDTESEAVVOVALDKARKGRTTIVIAHRLSTVRNADVIAG 600
Db 541 IARALVENPKILLDEATSDALDTESEAVVOVALDKARKGRTTIVIAHRLSTVRNADVIAG 600
Qy 601 FDDGVIYKGNHDELMKEGKIYFKLVMTQTAGNEVELENADESKSIDALEMSSNDRS 660
Db 601 FDDGVIYKGNHDELMKEGKIYFKLVMTQTAGNEVELENADESKSIDALEMSSNDRS 660
Qy 661 SLIKRSTRSVRSGOQDRKLSKEALDSEIPVPSFWRMKMLNLTWPVYVGVFCAL 720
Db 661 SLIKRSTRSVRSGOQDRKLSKEALDSEIPVPSFWRMKMLNLTWPVYVGVFCAL 720
Qy 721 NGGLQPAFAIIFSKIIIGVFRIDDPETKRONSNLFSLLFLALGIIISITFFLQFTFGKA 780
Db 721 NGGLQPAFAIIFSKIIIGVFRIDDPETKRONSNLFSLLFLALGIIISITFFLQFTFGKA 780
Qy 781 GEILTUKRLRYVFRSMRLQDVSWPDDPKNTTGALTTLANDAAQVKAIGSRSLAVITONI 840
Db 781 GEILTUKRLRYVFRSMRLQDVSWPDDPKNTTGALTTLANDAAQVKAIGSRSLAVITONI 840
Qy 841 ANLGTGIIISFIVGMQTLTLLALVPIIATAGVEMKMLSGOALKDKKELEGAGKIAATEA 900
Db 841 ANLGTGIIISFIVGMQTLTLLALVPIIATAGVEMKMLSGOALKDKKELEGAGKIAATEA 900
Qy 901 IENFRTVSLTQEQKFEMHYAQSLQVPRNSLRKAHIFGITFSFTQAMMYFSYAGCPRFG 960
Db 901 IENFRTVSLTQEQKFEMHYAQSLQVPRNSLRKAHIFGITFSFTQAMMYFSYAGCPRFG 960
Qy 961 AYLVAHKLMSEFEDVLLVFSVAVFGAMAVGVSSPAPDYAKAKISAHHIMIEKTPILDS 1020
Db 961 AYLVAHKLMSEFEDVLLVFSVAVFGAMAVGVSSPAPDYAKAKISAHHIMIEKTPILDS 1020
Qy 1021 YSTEGMLPNTLEGNTVFEVVFNTPRDPDIPVLQGLSLEVKKGOTLALVGSSGCGKSTTV 1080
Db 1021 YSTEGMLPNTLEGNTVFEVVFNTPRDPDIPVLQGLSLEVKKGOTLALVGSSGCGKSTTV 1080
Qy 1081 QLLERFYDPLAGKYLVDGKEIKRLNVQWLAHGLIVSQEPILPDCSIAENIAYGDNRRV 1140
Db 1081 QLLERFYDPLAGKYLVDGKEIKRLNVQWLAHGLIVSQEPILPDCSIAENIAYGDNRRV 1140
Qy 1141 SOBEIVRAAKEANTHAFIESLPNKYSTKVGDKGTQSGGOKORIAIARALVRPHILLD 1200
Db 1141 SOBEIVRAAKEANTHAFIESLPNKYSTKVGDKGTQSGGOKORIAIARALVRPHILLD 1200
Qy 1201 EATSALDTESEKVVQEAALDKAREGRTTIVIAHRLSTIQNADLIWVFONGRVEKHGTHQOL 1260
Db 1201 EATSALDTESEKVVQEAALDKAREGRTTIVIAHRLSTIQNADLIWVFONGRVEKHGTHQOL 1260
Qy 1261 LAQGIYFMSVSVQAGTKRQ 1280
Db 1261 LAQGIYFMSVSVQAGTKRQ 1280

RESULT 7

US-08-583-276-19

; Sequence 19, Application US/08583276

; Patent No. 5837536

; GENERAL INFORMATION:

; APPLICANT: McDonagh, Kevin T.

; APPLICANT: Nienhuis, Arthur

; APPLICANT: Tolstochev, Paul

; TITLE OF INVENTION: IMPROVED EXPRESSION OF HUMAN

; TITLE OF INVENTION: MULTIDRUG RESISTANCE GENES AND IMPROVED

; TITLE OF INVENTION: SELECTION OF CELLS TRANSDUCED WITH SUCH GENES

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Carella, Byrne, Bain, Gilfillan,

; ADDRESSEE: Cecchi & Stewart

; STREET: 6 Becker Farm Road

; CITY: Roseland

; STATE: New Jersey

; COUNTRY: USA

; ZIP: 07068

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch diskette

; COMPUTER: IBM PS/2

; OPERATING SYSTEM: PC-DOS

; SOFTWARE: DW4.V2

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/583,276

; FILING DATE: 05-JAN-1996

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/332,444

; FILING DATE: 31-OCT-1994

; APPLICATION NUMBER: 07/897,712

; FILING DATE: 22-MAY-1992

; INFORMATION FOR SEQ ID NO: 19:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1280 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; MOLECULE TYPE:

; DESCRIPTION: protein

US-08-583-276-19

Query Match 99.9%; Score 6428; DB 1; Length 1280;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1279; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLEGDRNGGAKKKKFFKLNKSEKDKKPKTVSVFSMFRYSNNWLDKLYMVVGTAAII 60

Db 1 MLEGDRNGGAKKKKFFKLNKSEKDKKPKTVSVFSMFRYSNNWLDKLYMVVGTAAII 60

Qy 61 HGAGLPMLLVFGEEMTDIFANAGNLEDMSNITNRSINDTGFNNLBEDMTRYAYISG 120

Db 61 HGAGLPMLLVFGEEMTDIFANAGNLEDMSNITNRSINDTGFNNLBEDMTRYAYISG 120

Qy 121 IGAGLVAAIYQVSWFCLAAAGROIHKIRKQFFHATMROEIGWDFVDVDELNTRLTDDVS 180

Db 121 IGAGLVAAIYQVSWFCLAAAGROIHKIRKQFFHATMROEIGWDFVDVDELNTRLTDDVS 180

Qy 181 KINEVIGDKIGMFFQSMATFTGTGIVGTGKWKTLVLIALSPVLGSAVWAKILSSFT 240

Db 181 KINEVIGDKIGMFFQSMATFTGTGIVGTGKWKTLVLIALSPVLGSAVWAKILSSFT 240

Qy 241 DKELLAYAKAGAVAEVLAARTVIAFGGQKKELRYNKNLEAKRIGIKKAITANISIG 300

Db 241 DKELLAYAKAGAVAEVLAARTVIAFGGQKKELRYNKNLEAKRIGIKKAITANISIG 300

Qy 301 AAFLLIYASALAFWYGTTLVLSEYSGIVLTVPFVSLGAFSGVQASPSIEAFANARG 360

Db 301 AAFLLIYASALAFWYGTTLVLSEYSGIVLTVPFVSLGAFSGVQASPSIEAFANARG 360

Qy	1	MDLEGRNGGAKEKNFFKLNANKSKDKKERKPTVSVFSMPFRYSNWLDKLVYVVGTLAAII	60
Db	1	MDLEGRNGGAKEKNFFKLNANKSKDKKERKPTVSVFSMPFRYSNWLDKLVYVVGTLAAII	60
Qy	61	HGAGLPLMLVFGDWTDTFANAGNLGDLGALLFNNTNSNITDTPVWNLEEDMTRVAYY	120
Db	61	HGAGLPLMLVFGDWTDTFANAGNLGDLGALL---TNSNITDTPVWNLEEDMTRVAYY	117
Qy	121	YSGIGAGVLVAAYIQVSPFWCLAAGRQIHKIRKQFPHAIMRQIEIGWDFVDVHGYELNTRLTD	180
Db	118	YSGIGAGVLVAAYIQVSPFWCLAAGRQIHKIRKQFPHAIMRQIEIGWDFVDVHGYELNTRLTD	177
Qy	181	DVSKINREGIDKIGWFFQSMATPTTGFTVGTFRGWKLTLVILATSPVLGLSAAVWAKILS	240
Db	178	DVSKINREGIDKIGWFFQSMATPTTGFTVGTFRGWKLTLVILATSPVLGLSAAVWAKILS	237
Qy	241	SPTDKELLAVAKAGAVAEVLAAIRTVIAFGQKKELERYNNKLEBEAKRIGIKKAITANI	300
Db	238	SPTDKELLAVAKAGAVAEVLAAIRTVIAFGQKKELERYNNKLEBEAKRIGIKKAITANI	297
Qy	301	SIGAAFLLIYASYALAFWYGTTLVLSKEYSIGQVLTVFFSVYLIGAFSVGOASPSIEAPAN	360
Db	298	SIGAAFLLIYASYALAFWYGTTLVLSKEYSIGQVLTVFFSVYLIGAFSVGOASPSIEAPAN	357
Qy	361	ARGAAFEIPKIIDNKPSIDSVSKGHKPDNTKGNLEFRNVHFSYPSRKEVKILGMLKV	420
Db	358	ARGAAFEIPKIIDNKPSIDSVSKGHKPDNTKGNLEFRNVHFSYPSRKEVKILGMLKV	417
Qy	421	QSGQTVALVGNSGCGKSTTVQLMQRLYDPTGMSVSDGQDRTTNVFLREIIGVSGQEP	480
Db	418	QSGQTVALVGNSGCGKSTTVQLMQRLYDPTGMSVSDGQDRTTNVFLREIIGVSGQEP	477
Qy	481	VLFATTIAENIRYGREDVTWDEIEKAKEANAYDFIMKLPKQFDTLVGERGAQLSGGQKQ	540
Db	478	VLFATTIAENIRYGREDVTWDEIEKAKEANAYDFIMKLPKQFDTLVGERGAQLSGGQKQ	537
Qy	541	RIATAARALVRNPKILLIDBATSALDTSSEAVVQVALDKARKGRTTIVIAHRLSTVRNADV	600
Db	538	RIATAARALVRNPKILLIDBATSALDTSSEAVVQVALDKARKGRTTIVIAHRLSTVRNADV	597
Qy	601	IAGPDDGVIYVEKGNHDELMKEGYFKLVMTQAGNEIELENADESKSEIDTLEMSSH	660
Db	598	IAGPDDGVIYVEKGNHDELMKEGYFKLVMTQAGNEIELENADESKSEIDTLEMSSH	657
Qy	661	SGSSLIRKSTRSRVRSQGDRLKSTKEALDESIPVPSFWIRIMKMLNTEWPFYVVGVC	720
Db	658	SGSSLIRKSTRSRVRSQGDRLKSTKEALDESIPVPSFWIRIMKMLNTEWPFYVVGVC	717
Qy	721	AIINGGLQAPAVIFSKIIIGIFTRNDDBAETKRONSNLPSLLFLVLGIVSFITPFLQGTFF	780
Db	718	AIINGGLQAPAVIFSKIIIGIFTRNDDBAETKRONSNLPSLLFLVLGIVSFITPFLQGTFF	777
Qy	781	GKAGEIILTKRLRYMVFRSMLBODVSWFDDPKNTTGALTTRLANDAAQVKGAIISRILAIT	840
Db	778	GKAGEIILTKRLRYMVFRSMLBODVSWFDDPKNTTGALTTRLANDAAQVKGAIISRILAIT	837
Qy	841	QNIANLGTGIIISLYGHWLTLLLLAIVPIIAIAGVWEMKMLSGOALKDKKELESGAKIA	900
Db	838	QNIANLGTGIIISLYGHWLTLLLLAIVPIIAIAGVWEMKMLSGOALKDKKELESGAKIA	897
Qy	901	TEAIENFRTVVSLTQEQKFEHMYDOSLOQVPYRNSLRKAHIFGIIFTSFTOAMWFSYAGCF	960
Db	898	TEAIENFRTVVSLTQEQKFEHMYDOSLOQVPYRNSLRKAHIFGIIFTSFTOAMWFSYAGCF	957
Qy	961	RFGAYLVASHLMSFEDVLLVPSAVVFGMAVGOVSSFPADYAKAKVSAAHIMIIETKPL	1020
Db	958	RFGAYLVASHLMSFEDVLLVPSAVVFGMAVGOVSSFPADYAKAKVSAAHIMIIETKPL	1017
Qy	1021	IDSYSTEGLKPNTLEGNVTFNEVVFNTPTRLDIPVLQGLSLEVKKGTOLALVSGSGCGKS	1080
Db	1018	IDSYSTEGLKPNTLEGNVTFNEVVFNTPTRLDIPVLQGLSLEVKKGTOLALVSGSGCGKS	1077
Qy	1081	TVVOLLERFYDPLAGKVLDDGKEIKQLNVQWLRHGLIVSGEPIFLFDCSISENTAYGDNS	1140

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Db 1078 TVQLLERFYDP LAGKVLDDGKEIKQLNWMLRAHLGIVSQEPFLDDCSISENIATGDN5 1137
Qy 1141 RVVSEQEIVRAAKEANIHAIESLPNKYSYTRVGDKGTQLSGGQKQRIATARALVRQPHIL 1200
Db 1138 RVVSEQEIVRAAKEANIHAIESLPNKYSYTRVGDKGTQLSGGQKQRIATARALVRQPHIL 1197
Qy 1201 LLEATSALDTESEKVVQOEALDKARGRTCTIVIAHRLSTIONADLIIVFQNGRVKHEGTH 1260
Db 1198 LLEATSALDTESEKVVQOEALDKARGRTCTIVIAHRLSTIONADLIIVFQNGRVKHEGTH 1257
Qy 1261 QQLLAAKGIVFSVMVSVQAGAKRQ 1283
Db 1258 QQLLAAKGIVFSVMVSVQAGAKRQ 1280

RESULT 6
US-09-584-586-2
; Sequence 2, Application US/09584586
; Patent No. 6933150
; GENERAL INFORMATION:
; APPLICANT: Sorrentino, Brian
; APPLICANT: Bunting, Kevin
; TITLE OF INVENTION: EXPANSION OF HEMATOPOIETIC STEM CELLS TRANSDUCED WITH
; TITLE OF INVENTION: MDR-1 METHODS OF USE THEREOF
; FILE REFERENCE: 1340-1-021CIP
; CURRENT APPLICATION NUMBER: US/09/584,586
; CURRENT FILING DATE: 2000-05-31
; EARLIER APPLICATION NUMBER: US 60/086,988
; EARLIER FILING DATE: 1998-05-28
; EARLIER APPLICATION NUMBER: PCT/US99/11825
; EARLIER FILING DATE: 1999-05-27
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1280
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Human MDR 185-G
US-09-584-586-2

Query Match 96.4%; Score 6212.5; DB 2; Length 1280;
Best local Similarity 96.5%; Pred. No. 0;
Matches 1238; Conservative 18; Mismatches 24; Indels 3; Gaps 1;

Qy 1 MDLEGDRNGAEKKKPFKLNNKSKDKCKRKPVTVSVMFRYSNWLDKLYVMVGTLLAAII 60
Db 1 MDLEGDRNGAKKKNPFKLNNKSEKDKCKRKPVTVSVMFRYSNWLDKLYVMVGTLLAAII 60
Qy 61 HGAGLPLMLLVFGDMTDTTFANAGNLGDLGALLFNNTNSSNITDTPVWNLEEDMTRYAY 120
Db 61 HGAGLPLMLLVFGEMTDIFANAGLED---LMSNITNRSNDINDTGFPMNLEEDMTRYAY 117
Qy 121 YSGIGAGVLVAAYIQVSWFCLAGROIHKIRKQFFHAIIMRQEIQWDFDHDVGEINTRLTD 180
Db 118 YSGIGAGVLVAAYIQVSWFCLAGROIHKIRKQFFHAIIMRQEIQWDFDHDVGEINTRLTD 177
Qy 181 DVSKINEGIDKIGMFPQSQWATFPTGIVGFTGKWLTLVILAI5PVLGISAAMWAKILS 240
Db 178 DVSKINEGIDKIGMFPQSQWATFPTGIVGFTGKWLTLVILAI5PVLGISAAMWAKILS 237
Qy 241 SFTDKELLAYAKAGAAVEELAAIRTVIAFGGOKKELERYNKNLEBAKIGIKKAITANI 300
Db 238 SFTDKELLAYAKAGAAVEELAAIRTVIAFGGOKKELERYNKNLEBAKIGIKKAITANI 297
Qy 301 SIGAAFLIIYASVALAPWYGTTLVL5KESYISGOVLTVFFSVLIGASVGOASPIEAFAN 360
Db 298 SIGAAFLIIYASVALAFWYGTTLVL5KESYISGOVLTVFFSVLIGASVGOASPIEAFAN 357
Qy 361 ARGAAFEI PKIINDKESIDSYKSGHKPDNIKNLEFRNVHPSYPSRKEVKILKGLNLKV 420
Db 358 ARGAAFEI PKIINDKESIDSYKSGHKPDNIKNLEFRNVHPSYPSRKEVKILKGLNLKV 417

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421 QSGQTVLVGNSGCGKSTTVQLMQRLYDPTGMSVSDGQDINTINVRFLREIIGVVSQBP 480
418 QSGQTVLVGNSGCGKSTTVQLMQRLYDPTGMSVSDGQDINTINVRFLREIIGVVSQBP 477
481 VLFATTIAENIRYGRDVTMDIEKAVKEANAYDFIMKLPOKFDTLVGERGQALSGGQKQ 540
478 VLFATTIAENIRYGRDVTMDIEKAVKEANAYDFIMKLPOKFDTLVGERGQALSGGQKQ 537
541 RIAIARALVRNPKILLDEATSALETSALDTESEAVVQVQALDKARKGRTTIVIAHRLSTVRNADV 600
538 RIAIARALVRNPKILLDEATSALETSALDTESEAVVQVQALDKARKGRTTIVIAHRLSTVRNADV 597
601 IAGFDGTVIVEKGNHDELMKEGIYFKLVMTQAGNEIELENAADESKSEIDTLEMSHD 660
598 IAGFDGTVIVEKGNHDELMKEGIYFKLVMTQAGNEIELENAADESKSEIDTLEMSHD 657
661 SSSLIKRESTRSRVRSVRSQQRKLTKEALDESIPVSWFRIMKLNLTWEPYFVVGVC 720
658 SRSSLIKRESTRSRVRSVRSQQRKLTKEALDESIPVSWFRIMKLNLTWEPYFVVGVC 717
721 AIINGLOPAPAVIFSKIIIGVTRIDDPETKQNSNLSFLLFLALGIIISFIIFLQGF 780
718 AIINGLOPAPAVIFSKIIIGVTRIDDPETKQNSNLSFLLFLALGIIISFIIFLQGF 777
781 GKAGELTKRLRYWFRSMRLQDVSWFDDPKNTTGATTLRLANDAAQVGAIGSLAIIIT 840
778 GKAGELTKRLRYWFRSMRLQDVSWFDDPKNTTGATTLRLANDAAQVGAIGSLAIIIT 837
841 QNIANLGTGIIISLIYWGQVTLTLLLAIVPIIAIAGVVENKMLSGQALKDKKLEAGAKIA 900
838 QNIANLGTGIIISLIYWGQVTLTLLLAIVPIIAIAGVVENKMLSGQALKDKKLEAGAKIA 897
901 TEAIENFRVTSLTQOKHEHYDQSLQVPRYSIRKAHIFGTFSTQAMMYFSYAGCF 960
898 TEAIENFRVTSLTQOKHEHYDQSLQVPRYSIRKAHIFGTFSTQAMMYFSYAGCF 957
961 RFGAYLVHLSMFEDVLVFSVAVFGAMAVGVSSFPADYAKAKYSAAHIIIMIEKTP 1020
958 RFGAYLVHLSMFEDVLVFSVAVFGAMAVGVSSFPADYAKAKYSAAHIIIMIEKTP 1017
1021 IDSYSTGLKPNTEGNTVFNEVFNPTRLDIPVLQGLSLEVKVQGTALVGSQCGK 1080
1018 IDSYSTGLKPNTEGNTVFNEVFNPTRLDIPVLQGLSLEVKVQGTALVGSQCGK 1077
1081 TVVQLLERYDPLAGKVLDDGKEIKOLNVQWLBRAHIGIYVSOEPIILFDCSISENIAYGDS 1140
1078 TVVQLLERYDPLAGKVLDDGKEIKOLNVQWLBRAHIGIYVSOEPIILFDCSISENIAYGDS 1137
1141 RVVSOEIVRAAKEANIHAFIESLPNKYSTRVGDKGTQLSGGQKORIAIARALVRPHIL 1200
1138 RVVSOEIVRAAKEANIHAFIESLPNKYSTRVGDKGTQLSGGQKORIAIARALVRPHIL 1197
1201 LIDEATSALETSALDTESEAVVQVQALDKARKGRTTIVIAHRLSTVRNADV 1260
1198 LIDEATSALETSALDTESEAVVQVQALDKARKGRTTIVIAHRLSTVRNADV 1257
1261 QQLLAOKGIYFMSVQAGAKRQ 1283
1258 QQLLAOKGIYFMSVQAGAKRQ 1280

RESULT 7
US-09-767-594-2
Sequence 2, Application US/09767594
Patent No. 6521635
GENERAL INFORMATION:
APPLICANT: Bates, Susan
APPLICANT: Robey, Robert
APPLICANT: The Government of the United States of America
APPLICANT: as represented by the Secretary of the
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Inhibition of MXR Transport by Acridine Derivatives

FILE REFERENCE: 015280-402100US
CURRENT APPLICATION NUMBER: US/09/767,594
CURRENT FILING DATE: 2001-01-22
PRIOR APPLICATION NUMBER: US 60/177,410
PRIOR FILING DATE: 2000-01-20
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patent in Ver. 2.1
SEQ ID NO 2
LENGTH: 1280
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: human P-glycoprotein (Pgp)/multi-drug resistance 1
OTHER INFORMATION: (Mdr-1) ATP-binding cassette (ABC transporter)
OTHER INFORMATION: protein
US-09-767-594-2

Query Match 96.3%; Score 6203.5; DB 2; Length 1280;
Best Local Similarity 96.4%; Pred. No. 0;
Matches 1237; Conservative 18; Mismatches 25; Indels 3; Gaps 1;

QY 1 MDLEGRNGCAEKKNFFKLNKSKKDKKERKPTVSVFMSFRYSNWLDKLYMVVGTAAII 60
DB 1 MDLEGRNGCAEKKNFFKLNKSKKDKKERKPTVSVFMSFRYSNWLDKLYMVVGTAAII 60
QY 61 HGAGLPLMLVFGDMTDTFANAGNIGDGLGALLFNNTSSNITDTPVNVNLEBDMTRYAY 120
DB 61 HGAGLPLMLVFGDMTDTFANAGNIGDGLGALLFNNTSSNITDTPVNVNLEBDMTRYAY 117
QY 121 YSGIGAGVLAAYIQVSWFCLAAAGQIHKIRKQFPHAMROEIGWDFVHDVDELNTRLTD 180
DB 118 YSGIGAGVLAAYIQVSWFCLAAAGQIHKIRKQFPHAMROEIGWDFVHDVDELNTRLTD 177
QY 181 DVSKINEGIDKIGNFFQSMATFFTGIVGTRGKLTLLVLAISPVLGSAVWAKILS 240
DB 178 DVSKINEGIDKIGNFFQSMATFFTGIVGTRGKLTLLVLAISPVLGSAVWAKILS 237
QY 241 SFTDKELLAYAKAGAVABEVLAARITVIAFGOKKELERYKNKLEBAKIGIKKAITANI 300
DB 238 SFTDKELLAYAKAGAVABEVLAARITVIAFGOKKELERYKNKLEBAKIGIKKAITANI 297
QY 301 SIGAFLIYASALAFYVGTTLVLSKEYSISGOVLTVPFVSVLIGAFSGQASPSIEAFAN 360
DB 298 SIGAFLIYASALAFYVGTTLVLSKEYSISGOVLTVPFVSVLIGAFSGQASPSIEAFAN 357
QY 361 ARGAAFEIYFKIIDNKPSIDSYSGHKPDNIKGNLEFRNVHFSYPSRKEVKILKGLNLKV 420
DB 358 ARGAAFEIYFKIIDNKPSIDSYSGHKPDNIKGNLEFRNVHFSYPSRKEVKILKGLNLKV 417
QY 421 QSGQTVLVGNSGCGKSTTVQLMQRLYDPTGMSVSDGQDINTINVRFLREIIGVVSQBP 480
DB 418 QSGQTVLVGNSGCGKSTTVQLMQRLYDPTGMSVSDGQDINTINVRFLREIIGVVSQBP 477
QY 481 VLFATTIAENIRYGRDVTMDIEKAVKEANAYDFIMKLPOKFDTLVGERGQALSGGQKQ 540
DB 478 VLFATTIAENIRYGRDVTMDIEKAVKEANAYDFIMKLPOKFDTLVGERGQALSGGQKQ 537
QY 541 RIAIARALVRNPKILLDEATSALETSALDTESEAVVQVQALDKARKGRTTIVIAHRLSTVRNADV 600
DB 538 RIAIARALVRNPKILLDEATSALETSALDTESEAVVQVQALDKARKGRTTIVIAHRLSTVRNADV 597
QY 601 IAGFDGTVIVEKGNHDELMKEGIYFKLVMTQAGNEIELENAADESKSEIDTLEMSHD 660
DB 598 IAGFDGTVIVEKGNHDELMKEGIYFKLVMTQAGNEIELENAADESKSEIDTLEMSHD 657
QY 661 SSSLIKRESTRSRVRSVRSQQRKLTKEALDESIPVSWFRIMKLNLTWEPYFVVGVC 720
DB 658 SRSSLIKRESTRSRVRSVRSQQRKLTKEALDESIPVSWFRIMKLNLTWEPYFVVGVC 717
QY 721 AIINGLOPAPAVIFSKIIIGVTRIDDPETKQNSNLSFLLFLALGIIISFIIFLQGF 780
DB 718 AIINGLOPAPAVIFSKIIIGVTRIDDPETKQNSNLSFLLFLALGIIISFIIFLQGF 777

Query Match 96.3%; Score 6203.5; DB 2; Length 1280;
Best Local Similarity 96.4%; Pred. No. 0;
Matches 1237; Conservative 18; Mismatches 25; Indels 3; Gaps 1;

QY 1 MDLEGRNGGAKGNPFKLNKSKDKKPKTVSFMFRYSNMWLDKLYMVVGTAAII 60
DB 1 MDLEGRNGGAKGNPFKLNKSKDKKPKTVSFMFRYSNMWLDKLYMVVGTAAII 60
QY 61 HGAGLPLMMLVFGDMTDTFANAGNLGDLGALLFNNTNSNIITDTPVMNLEEDMTRYAY 120
DB 61 HGAGLPLMMLVFGDMTDTFANAGNLGDLGALLFNNTNSNIITDTPVMNLEEDMTRYAY 117
QY 121 YSGIGAGVLVAAYIQVSFWCLAGROIHKIQFPHAIMRQEIIGWDFDHDVHGLNTRLTD 180
DB 118 YSGIGAGVLVAAYIQVSFWCLAGROIHKIQFPHAIMRQEIIGWDFDHDVHGLNTRLTD 177
QY 181 DVSKEINIEGDKIMGFQSMATPFTGFI VGTFRGWKLTIVILAI SPVLGLSAVWAKILS 240
DB 178 DVSKEINIEGDKIMGFQSMATPFTGFI VGTFRGWKLTIVILAI SPVLGLSAVWAKILS 237
QY 241 SFTDKELLAYAKAGAAVEVLAAIRTVIAFGGOKKELRYNKNLEAKIGIKKAITANI 300
DB 238 SFTDKELLAYAKAGAAVEVLAAIRTVIAFGGOKKELRYNKNLEAKIGIKKAITANI 297
QY 301 SIGAPELLIYASVALAFWYGTTLVLVLSKEYSIGQVLTVPFVSVLIGAFSVGOASPSIEAFAN 360
DB 298 SIGAPELLIYASVALAFWYGTTLVLVLSKEYSIGQVLTVPFVSVLIGAFSVGOASPSIEAFAN 357
QY 361 ARGAAVEIFKIIDNKPSIDSYSGSKHPDNKGNLEFRNVHFSYPSRKEVKILKGNLKV 420
DB 358 ARGAAVEIFKIIDNKPSIDSYSGSKHPDNKGNLEFRNVHFSYPSRKEVKILKGNLKV 417
QY 421 QSGQTVLVNCSGCKSTTVLMQRLYDPTGEMVSDGDIRINVRFLREIIGVVSQEP 480
DB 418 QSGQTVLVNCSGCKSTTVLMQRLYDPTGEMVSDGDIRINVRFLREIIGVVSQEP 477
QY 481 VLPATTIAENIRYGRDVTMDTEKAVKEANAYDFIMKLPQKPTDVLVGERGAOLSGQKQ 540
DB 478 VLPATTIAENIRYGRDVTMDTEKAVKEANAYDFIMKLPQKPTDVLVGERGAOLSGQKQ 537
QY 541 RIAIARALVRNPKILLDEATSDALDTESEAVQVVALDKARKGRTTIVIAHRLSTVRNADV 600
DB 538 RIAIARALVRNPKILLDEATSDALDTESEAVQVVALDKARKGRTTIVIAHRLSTVRNADV 597
QY 601 IAGFDGVIKGNHDELMKEGIFKLVMTQTAGNEIELENAADSKSIDTLEMSSH 660
DB 598 IAGFDGVIKGNHDELMKEGIFKLVMTQTAGNEIELENAADSKSIDTLEMSSH 657
QY 661 SGSSLRKSTRSVRSGQDRKLSLTKALDESIPPVSWFRIMKLNLTWPFYVGVFC 720
DB 658 SRSLRKSTRSVRSGQDRKLSLTKALDESIPPVSWFRIMKLNLTWPFYVGVFC 717
QY 721 AIINGLOPAVAFISKIIIGITRNDADYKRONSNLFSLLFLVLGVISFITPFGQFTF 780
DB 718 AIINGLOPAVAFISKIIIGITRNDADYKRONSNLFSLLFLVLGVISFITPFGQFTF 777
QY 781 GKAGEILTCLRMYVPSMLRODVSFDDPKNTGTALTTLANDAAVKGAISRLAIIT 840
DB 778 GKAGEILTCLRMYVPSMLRODVSFDDPKNTGTALTTLANDAAVKGAISRLAIIT 837
QY 841 QNTANLGTGIIISLYGWQLTLLALLAIVPIIAIAGVVMKMLSGQALKDKKELEGAKIA 900
DB 838 QNTANLGTGIIISLYGWQLTLLALLAIVPIIAIAGVVMKMLSGQALKDKKELEGAKIA 897
QY 901 TEAIENFRVTVSLTQEQFHEMYDQSLQVPRNSLRKAHIFGITFTSFTQAMMYSYAGCF 960
DB 898 TEAIENFRVTVSLTQEQFHEMYDQSLQVPRNSLRKAHIFGITFTSFTQAMMYSYAGCF 957
QY 961 RFGAYLVHSLMSPEDVLLVFSVAVFGMAVGVSSFAPDYAKAKVSAAHIMIEKTPL 1020
DB 958 RFGAYLVHSLMSPEDVLLVFSVAVFGMAVGVSSFAPDYAKAKVSAAHIMIEKTPL 1017
QY 1021 IDSYSTEGLKNTLEGNTVFNVTPTDIPVLQGLSLEVKKGTALVGSSEGCCKS 1080

1018 IDSYSTEGLKNTLEGNTVFNVTPTDIPVLQGLSLEVKKGTALVGSSEGCCKS 1077
1081 TVVQLLEFYDPLAGKVLDDGKEIKQLNVQWMLRAHLGIVSQEPILFDCSISENTIAYGNS 1140
1078 TVVQLLEFYDPLAGKVLDDGKEIKQLNVQWMLRAHLGIVSQEPILFDCSISENTIAYGNS 1137
1141 RVVSEIEIVRAAKENIHAFTESLNPKNYSTRVGDKGTOLSGGOKORIAIARALVROPHTL 1200
1138 RVVSEIEIVRAAKENIHAFTESLNPKNYSTRVGDKGTOLSGGOKORIAIARALVROPHTL 1197
1201 LIDEATSDALDTESEKVOEALDKAREGTCIVIAHRLSTIQNADLIVVFQNGRVKHEGTH 1260
1198 LIDEATSDALDTESEKVOEALDKAREGTCIVIAHRLSTIQNADLIVVFQNGRVKHEGTH 1257
1261 QOLLAQKGIYFSWVSVOAGAKRQ 1283
1258 QOLLAQKGIYFSWVSVOAGAKRQ 1280

RESULT 11
US-09-817-762-3
Sequence 3, Application US/09817762
Patent No. 6858774
GENERAL INFORMATION
APPLICANT: Spalding, Edgar P.
APPLICANT: No. 6858774, Bostl
TITLE OF INVENTION: MDR-Like ABC Transporter Gene From
TITLE OF INVENTION: Plants
FILE REFERENCE: 13238-00061
CURRENT APPLICATION NUMBER: US/09/817,762
PRIOR FILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: PCT/US99/22363
PRIOR FILING DATE: 1999-09-24
PRIOR APPLICATION NUMBER: US 60/101,814
PRIOR FILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 1280
TYPE: PRT
ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: Genbank P08183
DATABASE ENTRY DATE: 1997-11-01
US-09-817-762-3

Query Match 96.3%; Score 6203.5; DB 2; Length 1280;
Best Local Similarity 96.4%; Pred. No. 0;
Matches 1237; Conservative 18; Mismatches 25; Indels 3; Gaps 1;

QY 1 MDLEGRNGGAKGNPFKLNKSKDKKPKTVSFMFRYSNMWLDKLYMVVGTAAII 60
DB 1 MDLEGRNGGAKGNPFKLNKSKDKKPKTVSFMFRYSNMWLDKLYMVVGTAAII 60
QY 61 HGAGLPLMMLVFGDMTDTFANAGNLGDLGALLFNNTNSNIITDTPVMNLEEDMTRYAY 120
DB 61 HGAGLPLMMLVFGDMTDTFANAGNLGDLGALLFNNTNSNIITDTPVMNLEEDMTRYAY 117
QY 121 YSGIGAGVLVAAYIQVSFWCLAGROIHKIQFPHAIMRQEIIGWDFDHDVHGLNTRLTD 180
DB 118 YSGIGAGVLVAAYIQVSFWCLAGROIHKIQFPHAIMRQEIIGWDFDHDVHGLNTRLTD 177
QY 181 DVSKEINIEGDKIMGFQSMATPFTGFI VGTFRGWKLTIVILAI SPVLGLSAVWAKILS 240
DB 178 DVSKEINIEGDKIMGFQSMATPFTGFI VGTFRGWKLTIVILAI SPVLGLSAVWAKILS 237
QY 241 SFTDKELLAYAKAGAAVEVLAAIRTVIAFGGOKKELRYNKNLEAKIGIKKAITANI 300
DB 238 SFTDKELLAYAKAGAAVEVLAAIRTVIAFGGOKKELRYNKNLEAKIGIKKAITANI 297
QY 301 SIGAPELLIYASVALAFWYGTTLVLVLSKEYSIGQVLTVPFVSVLIGAFSVGOASPSIEAFAN 360
DB 298 SIGAPELLIYASVALAFWYGTTLVLVLSKEYSIGQVLTVPFVSVLIGAFSVGOASPSIEAFAN 357
QY 361 ARGAAVEIFKIIDNKPSIDSYSGSKHPDNKGNLEFRNVHFSYPSRKEVKILKGNLKV 420
DB 358 ARGAAVEIFKIIDNKPSIDSYSGSKHPDNKGNLEFRNVHFSYPSRKEVKILKGNLKV 417
QY 421 QSGQTVLVNCSGCKSTTVLMQRLYDPTGEMVSDGDIRINVRFLREIIGVVSQEP 480
DB 418 QSGQTVLVNCSGCKSTTVLMQRLYDPTGEMVSDGDIRINVRFLREIIGVVSQEP 477
QY 481 VLPATTIAENIRYGRDVTMDTEKAVKEANAYDFIMKLPQKPTDVLVGERGAOLSGQKQ 540
DB 478 VLPATTIAENIRYGRDVTMDTEKAVKEANAYDFIMKLPQKPTDVLVGERGAOLSGQKQ 537
QY 541 RIAIARALVRNPKILLDEATSDALDTESEAVQVVALDKARKGRTTIVIAHRLSTVRNADV 600
DB 538 RIAIARALVRNPKILLDEATSDALDTESEAVQVVALDKARKGRTTIVIAHRLSTVRNADV 597
QY 601 IAGFDGVIKGNHDELMKEGIFKLVMTQTAGNEIELENAADSKSIDTLEMSSH 660
DB 598 IAGFDGVIKGNHDELMKEGIFKLVMTQTAGNEIELENAADSKSIDTLEMSSH 657
QY 661 SGSSLRKSTRSVRSGQDRKLSLTKALDESIPPVSWFRIMKLNLTWPFYVGVFC 720
DB 658 SRSLRKSTRSVRSGQDRKLSLTKALDESIPPVSWFRIMKLNLTWPFYVGVFC 717
QY 721 AIINGLOPAVAFISKIIIGITRNDADYKRONSNLFSLLFLVLGVISFITPFGQFTF 780
DB 718 AIINGLOPAVAFISKIIIGITRNDADYKRONSNLFSLLFLVLGVISFITPFGQFTF 777
QY 781 GKAGEILTCLRMYVPSMLRODVSFDDPKNTGTALTTLANDAAVKGAISRLAIIT 840
DB 778 GKAGEILTCLRMYVPSMLRODVSFDDPKNTGTALTTLANDAAVKGAISRLAIIT 837
QY 841 QNTANLGTGIIISLYGWQLTLLALLAIVPIIAIAGVVMKMLSGQALKDKKELEGAKIA 900
DB 838 QNTANLGTGIIISLYGWQLTLLALLAIVPIIAIAGVVMKMLSGQALKDKKELEGAKIA 897
QY 901 TEAIENFRVTVSLTQEQFHEMYDQSLQVPRNSLRKAHIFGITFTSFTQAMMYSYAGCF 960
DB 898 TEAIENFRVTVSLTQEQFHEMYDQSLQVPRNSLRKAHIFGITFTSFTQAMMYSYAGCF 957
QY 961 RFGAYLVHSLMSPEDVLLVFSVAVFGMAVGVSSFAPDYAKAKVSAAHIMIEKTPL 1020
DB 958 RFGAYLVHSLMSPEDVLLVFSVAVFGMAVGVSSFAPDYAKAKVSAAHIMIEKTPL 1017
QY 1021 IDSYSTEGLKNTLEGNTVFNVTPTDIPVLQGLSLEVKKGTALVGSSEGCCKS 1080

Db 298 SIGAAFLLIYASALAFWYGTTLVLSEYSGVLTVPFSSVLIGAFSVGQASPSIEAFAN 357
 QY 361 ARGAAFEIPIKIIDNKPSIDSYSGHGPNDIKGNLEFRNVHFSYPSRKEVKILGKLNKV 420
 Db 358 ARGAAFEIPIKIIDNKPSIDSYSGHGPNDIKGNLEFRNVHFSYPSRKEVKILGKLNKV 417
 QY 421 QSGQTVALVNGSGCGKSTTVQLMQRLYDPTGEMVSDGQDRTINVRFLREIIGVVSQEP 480
 Db 418 QSGQTVALVNGSGCGKSTTVQLMQRLYDPTGEMVSDGQDRTINVRFLREIIGVVSQEP 477
 QY 481 VLFATTIAENIRYGRDVTWDEIEKAVKEANAYDFIMKLPKQFDTLVGERGAOLSGGQK 540
 Db 478 VLFATTIAENIRYGRDVTWDEIEKAVKEANAYDFIMKLPKQFDTLVGERGAOLSGGQK 537
 QY 541 RIAIARALVRNPKILLDEATSAIDTSEAVVQVQALDKARKGRTTIVIAHRLSTVRNADV 600
 Db 538 RIAIARALVRNPKILLDEATSAIDTSEAVVQVQALDKARKGRTTIVIAHRLSTVRNADV 597
 QY 601 IAGFDGVIIVEKGNHDELMKEGTYFKLVMTQTAGNEIELENADESKSEIDTLEMSHD 660
 Db 598 IAGFDGVIIVEKGNHDELMKEGTYFKLVMTQTAGNEIELENADESKSEIDTLEMSHD 657
 QY 661 SGSSLRKSTRSRVRSGSQDRLKSTKEALDESIPPVSWFRIMKLNLTWPFVVGVC 720
 Db 658 SRSSLRKSTRSRVRSGSQDRLKSTKEALDESIPPVSWFRIMKLNLTWPFVVGVC 717
 QY 721 AIINGLOPAPAVIFSKIIGITFRNDDAETKRONSLFSLFLVLGIVSITTFPLOGFTF 780
 Db 718 AIINGLOPAPAVIFSKIIGITFRNDDAETKRONSLFSLFLVLGIVSITTFPLOGFTF 777
 QY 781 GKAGEITLTKELRYMVFESMLRQDVSFDDPKNTTGALTTLANDAAQVKAIGSLIAIT 840
 Db 778 GKAGEITLTKELRYMVFESMLRQDVSFDDPKNTTGALTTLANDAAQVKAIGSLIAIT 837
 QY 841 QNIANLGTGIIISLIYQWQTLTLLLAIVPIIATAGVVMEMKLSQALDKKELEGAKIA 900
 Db 838 QNIANLGTGIIISLIYQWQTLTLLLAIVPIIATAGVVMEMKLSQALDKKELEGAKIA 897
 QY 901 TEAIENFRVVSUTQEQKFEHMYDQSLQVPRNSLRKAHIFGITFTQAMVFSYAGCF 960
 Db 898 TEAIENFRVVSUTQEQKFEHMYDQSLQVPRNSLRKAHIFGITFTQAMVFSYAGCF 957
 QY 961 RFCAIYVAHLSMFEDVLLVFSVAVFGAMAVGVSSPAPDYAKAKYSAAHIMLIEKTP 1020
 Db 958 RFCAIYVAHLSMFEDVLLVFSVAVFGAMAVGVSSPAPDYAKAKYSAAHIMLIEKTP 1017
 QY 1021 IDSISTEGLKPNTEGNTFNEVFNYPTRLDIPVLQGLSLEVKKGOTLALVSSGCGKS 1080
 Db 1018 IDSISTEGLKPNTEGNTFNEVFNYPTRLDIPVLQGLSLEVKKGOTLALVSSGCGKS 1077
 QY 1081 TVVQLLERFYDPLAGKVLIDGKEIKOLNVQWLAHLGIVSQEPILFDCSISENAYGDNS 1140
 Db 1078 TVVQLLERFYDPLAGKVLIDGKEIKOLNVQWLAHLGIVSQEPILFDCSISENAYGDNS 1137
 QY 1141 RVVSQSEIVRAAEKANTHAFIESLPNKYSFRVGDGKTLQSGGOKORTAIARALVRPHIL 1200
 Db 1138 RVVSQSEIVRAAEKANTHAFIESLPNKYSFRVGDGKTLQSGGOKORTAIARALVRPHIL 1197
 QY 1201 LLDEATSAIDTSEKVVQEAALDKAREGRTTCIVIAHRLSTTQNALDIIVFQNGRVKXGHT 1260
 Db 1198 LLDEATSAIDTSEKVVQEAALDKAREGRTTCIVIAHRLSTTQNALDIIVFQNGRVKXGHT 1257
 QY 1261 QLLAOKGIYFSMVSVQAGNRQ 1283
 Db 1258 QLLAOKGIYFSMVSVQAGNRQ 1280

RESULT 12

US-09-584-586-4

Sequence 4, Application US/09584586

Patent No. 6933150

GENERAL INFORMATION:

Applicant: Sorrentino, Brian

; APPLICANT: Bunting, Kevin
 ; TITLE OF INVENTION: EXPANSION OF HEMATOPOIETIC STEM CELLS TRANSDUCED WITH
 ; FILE OF INVENTION: MDR-1 METHODS OF USE THEREOF
 ; FILE REFERENCE: 1340-1-021CIP
 ; CURRENT APPLICATION NUMBER: US/09/584,586
 ; CURRENT FILING DATE: 2000-05-31
 ; EARLIER APPLICATION NUMBER: US 60/086,988
 ; EARLIER FILING DATE: 1998-05-28
 ; EARLIER APPLICATION NUMBER: PCT/US99/11825
 ; EARLIER FILING DATE: 1999-05-27
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO 4
 ; LENGTH: 1280
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: Human MDR 185-V
 ; US-09-584-586-4

Query Match 96.3%; Score 6203.5; DB 2; Length 1280;

Best Local Similarity 96.4%; Pred. No. 0;

Matches 1237; Conservative 18; Mismatches 25; Indels 3; Gaps 1;

QY 1 MDLEGRNGGAEGKKNFFKLNKSKDKKPKPTVSVFSPRYSNWLDKLYMVVGTLLAAII 60
 Db 1 MDLEGRNGGAEGKKNFFKLNKSKDKKPKPTVSVFSPRYSNWLDKLYMVVGTLLAAII 60
 QY 61 HGAGLPLMLLVFGDMTDTFANAGNLGDLGALLFNNTSSNITDTPVMNLEEDMTYAY 120
 Db 61 HGAGLPLMLLVFGDMTDTFANAGNLGDLGALLFNNTSSNITDTPVMNLEEDMTYAY 117
 QY 121 YSGIGAGVLVAAYIQVSWFCLAAGRQIHKIRKQFHAIMRQEIQWFDVHDVGEINLRLTD 180
 Db 118 YSGIGAGVLVAAYIQVSWFCLAAGRQIHKIRKQFHAIMRQEIQWFDVHDVGEINLRLTD 177
 QY 181 DVSKINEGIDGKIMGFQSMATFFTCFIVGFRGNKLTIVILAIISVLGSAVWAKILS 240
 Db 178 DVSKINEGIDGKIMGFQSMATFFTCFIVGFRGNKLTIVILAIISVLGSAVWAKILS 237
 QY 241 SFTDKELLAYAKAGAAVEVLAAIRFVIAFGGOKKELRYNKNLEAKRIGIKKAITANI 300
 Db 238 SFTDKELLAYAKAGAAVEVLAAIRFVIAFGGOKKELRYNKNLEAKRIGIKKAITANI 297
 QY 301 SIGAAFLLIYASALAFWYGTTLVLSEYSGVLTVPFSSVLIGAFSVGQASPSIEAFAN 360
 Db 298 SIGAAFLLIYASALAFWYGTTLVLSEYSGVLTVPFSSVLIGAFSVGQASPSIEAFAN 357
 QY 361 ARGAAFEIPIKIIDNKPSIDSYSGHGPNDIKGNLEFRNVHFSYPSRKEVKILGKLNKV 420
 Db 358 ARGAAFEIPIKIIDNKPSIDSYSGHGPNDIKGNLEFRNVHFSYPSRKEVKILGKLNKV 417
 QY 421 QSGQTVALVNGSGCGKSTTVQLMQRLYDPTGEMVSDGQDRTINVRFLREIIGVVSQEP 480
 Db 418 QSGQTVALVNGSGCGKSTTVQLMQRLYDPTGEMVSDGQDRTINVRFLREIIGVVSQEP 477
 QY 481 VLFATTIAENIRYGRDVTWDEIEKAVKEANAYDFIMKLPKQFDTLVGERGAOLSGGQK 540
 Db 478 VLFATTIAENIRYGRDVTWDEIEKAVKEANAYDFIMKLPKQFDTLVGERGAOLSGGQK 537
 QY 541 RIAIARALVRNPKILLDEATSAIDTSEAVVQVQALDKARKGRTTIVIAHRLSTVRNADV 600
 Db 538 RIAIARALVRNPKILLDEATSAIDTSEAVVQVQALDKARKGRTTIVIAHRLSTVRNADV 597
 QY 601 IAGFDGVIIVEKGNHDELMKEGTYFKLVMTQTAGNEIELENADESKSEIDTLEMSHD 660
 Db 598 IAGFDGVIIVEKGNHDELMKEGTYFKLVMTQTAGNEIELENADESKSEIDTLEMSHD 657
 QY 661 SGSSLRKSTRSRVRSGSQDRLKSTKEALDESIPPVSWFRIMKLNLTWPFVVGVC 720
 Db 658 SRSSLRKSTRSRVRSGSQDRLKSTKEALDESIPPVSWFRIMKLNLTWPFVVGVC 717
 QY 721 AIINGLOPAPAVIFSKIIGITFRNDDAETKRONSLFSLFLVLGIVSITTFPLOGFTF 780

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Db      1021  YSTEGMLPNTLEGNVTFGVFNYPTRDPDLPVLQGLSLEVKKGQTTALVGSSCGKSTVV 1080
Qy      1081  QLLERFYDPLAGKVLLDGKEIKQLANQWMLRAHLGIVSQEPILEDSCSISENIAYGDNRSVV 1140
Db      1081  QLLERFYDPLAGKVLLDGKEIKELNQLWMLRAHLGIVSQEPILEDSCSIAENIAYGDNRSVV 1140
Qy      1141  SQBEIVRAAKEANIHAIFIESLPNKYSTRVGDGKTQTLGGQKQRIATARALVROPHILLD 1200
Db      1141  SQBEIVRAAKEANIHAIFIESLPNKYSTKVGDGKTQTLGGQKQRIATARALVROPHILLD 1200
Qy      1201  EATSALDTESEKVVQALDKAREGRCTCIVIAHRLSTIQNADLIWVFQNGRVKXHGTHQOL 1260
Db      1201  EATSALDTESEKVVQALDKAREGRCTCIVIAHRLSTIQNADLIWVFQNGRVKXHGTHQOL 1260
Qy      1261  LAQGIYFMSVSVQAGAKRQ 1280
Db      1261  LAQGIYFMSVSVQAGTKRQ 1280

RESULT 11
US-09-817-762-3
; Sequence 3, Application US/09817762
; Patent No. 685874
; GENERAL INFORMATION:
; APPLICANT: Spalding, Edgar P.
; APPLICANT: No. 685874, Boel
; TITLE OF INVENTION: MDR-Like ABC Transporter Gene From
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 13238-00061
; CURRENT APPLICATION NUMBER: US/09/817,762
; CURRENT FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: PCT/US99/22363
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: US 60/101,814
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1280
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Genbank P08183
; DATABASE ENTRY DATE: 1997-11-01
US-09-817-762-3

Query Match          96.6%; Score 6209; DB 2; Length 1280;
Best Local Similarity 96.6%; Pred. No. 0;
Matches 1236; Conservative 19; Mismatches 25; Indels 0; Gaps 0;

Qy      1 MDLEGRNGAEEKKNFFKLNKSKDKCKRKPTVSVFSMFRYSNWLDKLYMVVGTLLAAII 60
Db      1 MDLEGRNGAKKKNFFKLNKSEKKDKCKRKPTVSVFSMFRYSNWLDKLYMVVGTLLAAII 60
Qy      61 HGAGLPLMLVFGDMTDTTFANAGNLGDLGALLTNSNITDTVPVMNLEEDMTYAYYSG 120
Db      61 HGAGLPLMLVFGEMTDIPFANAGNLEDSLMSNITNRSIDINDTGFPMNLEEDMTYAYYSG 120
Qy      121 IGAGVLVAAYIQVSFWCLAAAGROIHKIRQFFHAIIMROEIGWDFVDHVGELNRLTDDVS 180
Db      121 IGAGVLVAAYIQVSFWCLAAAGROIHKIRQFFHAIIMROEIGWDFVDHVGELNRLTDDVS 180
Qy      181 KINEGIGDKIGMFFQSQMAFTFTGFIYGFTRGWKLTLLVLAISPVLGLSAAVWAKILSSFT 240
Db      181 KINEVIGDKIGMFFQSQMAFTFTGFIYGFTRGWKLTLLVLAISPVLGLSAAVWAKILSSFT 240
Qy      241 DKELLAYAKAGAAEEVLAARTVIAFGGOKKELERYNKVLEAKRIGIKKAITANISIG 300
Db      241 DKELLAYAKAGAAEEVLAARTVIAFGGOKKELERYNKVLEAKRIGIKKAITANISIG 300
Qy      301 APFLIIYASVALAFWTGTTILVLSKEYSIGOVLTVFSSVLIGASVQASPSIEAFANRG 360

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301 AAFLLIYASALAFWYGTTLVLSGEYSIGQVLTVFFSVLIGAFSVGOQSPSIEAFANARG 360
361 AAFEIFKIIDNKPISDSYSGSHKPDNIKGNLEFRNVHFSYPSRKEVKILKGLNLKVQSG 420
361 AAFEIFKIIDNKPISDSYSGSHKPDNIKGNLEFRNVHFSYPSRKEVKILKGLNLKVQSG 420
421 QTVALVGNSSCGKSTTVQMLQRLYDPTGEMVSVGQDRTINVRFLREIIGVSOEPVLF 480
421 QTVALVGNSSCGKSTTVQMLQRLYDPTGEMVSVGQDRTINVRFLREIIGVSOEPVLF 480
481 ATTIAENIRYGRDVTWDEIEKAVKEANAYDFIMKLPKEDTLVGERGAQLSGGOKORIA 540
481 ATTIAENIRYGRDVTWDEIEKAVKEANAYDFIMKLPKEDTLVGERGAQLSGGOKORIA 540
541 IARALVRNPKILLDEATSEASALDTESEAVVQVALDKARKGRTTIVIAHRLSTVRNADVIAG 600
541 IARALVRNPKILLDEATSEASALDTESEAVVQVALDKARKGRTTIVIAHRLSTVRNADVIAG 600
601 FDDGVIVEKGNHDELMEKGIYFKLVMTQTAGNEIELENAADESKSEIDTLEMSSHDGSGS 660
601 FDDGVIVEKGNHDELMEKGIYFKLVMTQTAGNEIELENAADESKSEIDTLEMSSHDGSGS 660
661 SLIKRSTRSVRSGSQDRKSLSTKEALDESIIPVSVFWRIMKLNLTWPYFVGVFCALI 720
661 SLIKRSTRSVRSGSQDRKSLSTKEALDESIIPVSVFWRIMKLNLTWPYFVGVFCALI 720
721 NGGLQPAFAVIFSKIIGITFRNDADAETKRONSNLFSLLFLVLGIVSFTTFFLOQFTFGKA 780
721 NGGLQPAFAVIFSKIIGITFRNDADAETKRONSNLFSLLFLVLGIVSFTTFFLOQFTFGKA 780
781 GEILTKRLRYVFRSMLRQDVSFDDPKNTTGTALTRLANDAAQVKGAGISRLAIITONI 840
781 GEILTKRLRYVFRSMLRQDVSFDDPKNTTGTALTRLANDAAQVKGAGISRLAIITONI 840
841 ANLGTTIISLYGQWLTLLAIVPIITAIAGVEMKMLSGOALKDKKELSGAGKIA TEA 900
841 ANLGTTIISLYGQWLTLLAIVPIITAIAGVEMKMLSGOALKDKKELSGAGKIA TEA 900
901 IENFRVTVSLTQEQFHEMYDQSLQVPYRNSLRKAHIFGIFTFTQAMMYFSYAGCPRFG 960
901 IENFRVTVSLTQEQFHEMYDQSLQVPYRNSLRKAHIFGIFTFTQAMMYFSYAGCPRFG 960
961 AYLVAHLSMEDVLLVFSVAVFGMAVQVSSFPADYAKAKVSAAHIMIEKTPLIDS 1020
961 AYLVAHLSMEDVLLVFSVAVFGMAVQVSSFPADYAKAKVSAAHIMIEKTPLIDS 1020
1021 YSTGLKNTLEGNTVFNVEVFNPTPLDIPVQGLSLEVKKGTALVGSNGGCKSTVV 1080
1021 YSTGLKNTLEGNTVFNVEVFNPTPLDIPVQGLSLEVKKGTALVGSNGGCKSTVV 1080
1081 QLLERFYDPLAGKVLDDGKEIKOLNVQWLRHLGLIVSOEPIFLDCSISENTAYGDSRVV 1140
1081 QLLERFYDPLAGKVLDDGKEIKOLNVQWLRHLGLIVSOEPIFLDCSISENTAYGDSRVV 1140
1141 SQEIVRAAKANTHAFTESLPNKYSTRVGDKGTOLSGGQKORIAIARALVRQPHILLD 1200
1141 SQEIVRAAKANTHAFTESLPNKYSTRVGDKGTOLSGGQKORIAIARALVRQPHILLD 1200
1201 EATSALDTESEKVVQVQALDKAREGRTTIVIAHRLSTQNALDIYVFNQGRVKEHGTQOOL 1260
1201 EATSALDTESEKVVQVQALDKAREGRTTIVIAHRLSTQNALDIYVFNQGRVKEHGTQOOL 1260
1261 LAQGIYFSMVSVQAGAKRQ 1280
1261 LAQGIYFSMVSVQAGAKRQ 1280

RESULT 12

US-09-584-586-4
; Sequence 4, Application US/09584586
; Patent No: 6933150
; GENERAL INFORMATION:
; APPLICANT: Sorrentino, Brian

; APPLICANT: Bunting, Kevin
; TITLE OF INVENTION: EXPANSION OF HEMATOPOIETIC STEM CELLS TRANSDUCED WITH
; FILE REFERENCE: 1340-1-021CIP
; CURRENT APPLICATION NUMBER: US/09/584,586
; CURRENT FILING DATE: 2000-05-31
; EARLIER APPLICATION NUMBER: US 60/086,988
; EARLIER FILING DATE: 1998-05-28
; EARLIER APPLICATION NUMBER: PCT/US99/11825
; EARLIER FILING DATE: 1999-05-27
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 4
; LENGTH: 1280
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Human MDR 185-V
; US-09-584-586-4

Query Match 96.6%; Score 6209; DB 2; Length 1280;
Best Local Similarity 96.6%; Pred. No. 0;
Matches 1236; Conservative 19; Mismatches 25; Indels 0; Gaps 0;

Qy 1 MDLEGRNGGAEGKKNFPLANKSKKKKKKPTVSVFSPMRYSNWLDKLYMVGTLLAAII 60
Db 1 MDLEGRNGGAEGKKNFPLANKSKKKKKKPTVSVFSPMRYSNWLDKLYMVGTLLAAII 60
Qy 61 HGAGLPLMLVFGDMTDTFANAGNLGDLGALLTNSNITDTPVMNLEEDMTYAYVYSG 120
Db 61 HGAGLPLMLVFGDMTDTFANAGNLGDLGALLTNSNITDTPVMNLEEDMTYAYVYSG 120
Qy 121 IGAGLVAAIYQVSWFLAAGROIHRIKQFHAIRQEIQWDFDHDVDELNLTDDVS 180
Db 121 IGAGLVAAIYQVSWFLAAGROIHRIKQFHAIRQEIQWDFDHDVDELNLTDDVS 180
Qy 181 KINEGIDGKIMGFQSMATFTGTFVGTFRGKLTLLVILAIISVPLGLSAAVWAKILSSFT 240
Db 181 KINEGIDGKIMGFQSMATFTGTFVGTFRGKLTLLVILAIISVPLGLSAAVWAKILSSFT 240
Qy 241 DKELLAYAKAGAAVEEVLAAIRTVIAGGOKKELERKNKLEAKRIGIKKAITANISIG 300
Db 241 DKELLAYAKAGAAVEEVLAAIRTVIAGGOKKELERKNKLEAKRIGIKKAITANISIG 300
Qy 301 AAFLLIYASALAFWYGTTLVLSGEYSIGQVLTVFFSVLIGAFSVGOQSPSIEAFANARG 360
Db 301 AAFLLIYASALAFWYGTTLVLSGEYSIGQVLTVFFSVLIGAFSVGOQSPSIEAFANARG 360
Qy 361 AAFEIFKIIDNKPISDSYSGSHKPDNIKGNLEFRNVHFSYPSRKEVKILKGLNLKVQSG 420
Db 361 AAFEIFKIIDNKPISDSYSGSHKPDNIKGNLEFRNVHFSYPSRKEVKILKGLNLKVQSG 420
Qy 421 QTVALVGNSSCGKSTTVQMLQRLYDPTGEMVSVGQDRTINVRFLREIIGVSOEPVLF 480
Db 421 QTVALVGNSSCGKSTTVQMLQRLYDPTGEMVSVGQDRTINVRFLREIIGVSOEPVLF 480
Qy 481 ATTIAENIRYGRDVTWDEIEKAVKEANAYDFIMKLPKEDTLVGERGAQLSGGOKORIA 540
Db 481 ATTIAENIRYGRDVTWDEIEKAVKEANAYDFIMKLPKEDTLVGERGAQLSGGOKORIA 540
Qy 541 IARALVRNPKILLDEATSEASALDTESEAVVQVALDKARKGRTTIVIAHRLSTVRNADVIAG 600
Db 541 IARALVRNPKILLDEATSEASALDTESEAVVQVALDKARKGRTTIVIAHRLSTVRNADVIAG 600
Qy 601 FDDGVIVEKGNHDELMEKGIYFKLVMTQTAGNEIELENAADESKSEIDTLEMSSHDGSGS 660
Db 601 FDDGVIVEKGNHDELMEKGIYFKLVMTQTAGNEIELENAADESKSEIDTLEMSSHDGSGS 660
Qy 661 SLIKRSTRSVRSGSQDRKSLSTKEALDESIIPVSVFWRIMKLNLTWPYFVGVFCALI 720
Db 661 SLIKRSTRSVRSGSQDRKSLSTKEALDESIIPVSVFWRIMKLNLTWPYFVGVFCALI 720
Qy 721 NGGLQPAFAVIFSKIIGITFRNDADAETKRONSNLFSLLFLVLGIVSFTTFFLOQFTFGKA 780

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721 NGGLQPAFAIFSKIGVTRIDDPETKQNSLFLALGIISPTFFLQGFPGA 780
781 GEILTKRLRYMVRMLQDVSWFDDPKNTTCALTRLANDAAQVKGAGSLAIIQNI 840
781 GEILTKRLRYMVRMLQDVSWFDDPKNTTCALTRLANDAAQVKGAGSLAIIQNI 840
781 GEILTKRLRYMVRMLQDVSWFDDPKNTTCALTRLANDAAQVKGAGSLAIIQNI 840
841 ANLGTGIIISYIYQWLTLLAIIAIVPIIAIAGVVMKMLSGQALKDKKLEGGAGKATEA 900
841 ANLGTGIIISYIYQWLTLLAIIAIVPIIAIAGVVMKMLSGQALKDKKLEGGAGKATEA 900
901 IENERTVSLTQEQKFEHMYDQSLQVPRNSLRKAHIFGITTSFTQAMFYSGACFRFG 960
901 IENERTVSLTQEQKFEHMYDQSLQVPRNSLRKAHIFGITTSFTQAMFYSGACFRFG 960
961 AYLVAHSLMGFEDVLLVFSVAVFGAMAVGVSSFADYAKAKVSAAHIIIMIEKTPILDS 1020
961 AYLVAHSLMGFEDVLLVFSVAVFGAMAVGVSSFADYAKAKVSAAHIIIMIEKTPILDS 1020
1021 YSTGLKPNLTLEGNVTNEVVPYTRLDIPVLQGLSLEVKKGOTLALVSSGCGKSTVV 1080
1021 YSTGLKPNLTLEGNVTNEVVPYTRLDIPVLQGLSLEVKKGOTLALVSSGCGKSTVV 1080
1081 QLLERFYDPLAGKVLDDKGIKOLNVQWMLRAHLGIVSOEPIFDCSISENIAIYCDNSRVV 1140
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1141 SOBEIVRAAKEANHAHPIESLPNKYSYTRVCKGTOLSGGQKQRIATARALVROPHILLD 1200
1141 SOBEIVRAAKEANHAHPIESLPNKYSYTRVCKGTOLSGGQKQRIATARALVROPHILLD 1200
1201 EATSALDTESEKVVQEQALDKAREGRICIVIAHRLSTIQNADLIVFQNGRVEKHGTHOOL 1260
1201 EATSALDTESEKVVQEQALDKAREGRICIVIAHRLSTIQNADLIVFQNGRVEKHGTHOOL 1260
1261 LAQKGIYFMSVVOAGAKRQ 1280
1261 LAQKGIYFMSVVOAGAKRQ 1280

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RESULT 13
US-08-583-276-19
Sequence 19, Application US/08583276
Patent No. 5837536

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GENERAL INFORMATION:
APPLICANT: McDonagh, Kevin T.
APPLICANT: Nienhuis, Arthur
APPLICANT: Tolstoshev, Paul
TITLE OF INVENTION: IMPROVED EXPRESSION OF HUMAN
TITLE OF INVENTION: MULTIDRUG RESISTANCE GENES AND IMPROVED
TITLE OF INVENTION: SELECTION OF CELLS TRANSDUCED WITH SUCH GENES
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
ADDRESSEE: Cecchi & Stewart
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: New Jersey
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: DW4 V2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/583,276
FILING DATE: 05-JAN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/332,444
FILING DATE: 31-OCT-1994
APPLICATION NUMBER: 07/887,712

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; FILING DATE: 22-MAY-1992
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1280 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: protein
; US-08-583-276-19

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Query Match          96.5%; Score 6206; DB 1; Length 1280;
Best Local Similarity 96.5%; Pred. No. 0;
Matches 1235; Conservative 20; Mismatches 25; Indels 0; Gaps 0;

QY 1 MDLEGRNGAEKCNFKLNKSKDKKPKTVSVSMFPRYSNWLKLYMVGTTAAII 60
DB 1 MDLEGRNGAEKCNFKLNKSKDKKPKTVSVSMFPRYSNWLKLYMVGTTAAII 60
QY 61 HGAGLPLMLVFGDMTDTTFANAGNLGDLGALLTNSNITDTVPVNLLEEDMTYAYYSG 120
DB 61 HGAGLPLMLVFGDMTDTTFANAGNLGDLGALLTNSNITDTVPVNLLEEDMTYAYYSG 120
QY 121 IGAGVLVAAYIQVSWFCLAAAGRIHKKRQFHAIHQFIMRQEIHFVDFHVDVGLNTRLDVVS 180
DB 121 IGAGVLVAAYIQVSWFCLAAAGRIHKKRQFHAIHQFIMRQEIHFVDFHVDVGLNTRLDVVS 180
QY 181 KINEGIGDKIGMFQSMATFTTGFVGTTRGKLTIVILAIISPVGLSAAVWAKILSSPT 240
DB 181 KINEVIGDKIGMFQSMATFTTGFVGTTRGKLTIVILAIISPVGLSAAVWAKILSSPT 240
QY 241 DKELLAYAKAGAVEEVLAARTVIAFGQKKELRYNKNLEAKRIGIKKAITANISIG 300
DB 241 DKELLAYAKAGAVEEVLAARTVIAFGQKKELRYNKNLEAKRIGIKKAITANISIG 300
QY 301 AAFLLIYASYALAFWYGTTLVLSKYSYSGVLTVPFSSVLIAGFSVQASPSIEAFANARG 360
DB 301 AAFLLIYASYALAFWYGTTLVLSKYSYSGVLTVPFSSVLIAGFSVQASPSIEAFANARG 360
QY 361 AAFEFKIIDNKPSIDSYKSGHKPDNIKGNLEFRNVHFSYPSRKEVKILKGLNKKVQSG 420
DB 361 AAFEFKIIDNKPSIDSYKSGHKPDNIKGNLEFRNVHFSYPSRKEVKILKGLNKKVQSG 420
QY 421 QTVALVGNSSGCKSTTVQLMQRLYDPTGEMVSVGDQIRTNINVRFLRIIIGVVSQEPVLF 480
DB 421 QTVALVGNSSGCKSTTVQLMQRLYDPTGEMVSVGDQIRTNINVRFLRIIIGVVSQEPVLF 480
QY 481 ATTIAENIRYGRDVTWDEIEKAVKEANAYDFIMKLPKEDTLVGERGAQLSGGQKQRIA 540
DB 481 ATTIAENIRYGRDVTWDEIEKAVKEANAYDFIMKLPKEDTLVGERGAQLSGGQKQRIA 540
QY 541 IARALVRNPKILLDEATSDALDTESEAVVQALDKARKGRITTVIAHRLSTVRNADVIAG 600
DB 541 IARALVRNPKILLDEATSDALDTESEAVVQALDKARKGRITTVIAHRLSTVRNADVIAG 600
QY 601 FDDGVIIVEKGNHDELMKEGIIYFKLVMTQTAGNEIELENAADSKSIDTLEMSHSDSGS 660
DB 601 FDDGVIIVEKGNHDELMKEGIIYFKLVMTQTAGNEIELENAADSKSIDTLEMSHSDSGS 660
QY 661 SLIRKSTRSVRGSGQDRKLTSTKALDESIPVSVFWRIMKLNLTWPYFVVGVCFAII 720
DB 661 SLIRKSTRSVRGSGQDRKLTSTKALDESIPVSVFWRIMKLNLTWPYFVVGVCFAII 720
QY 721 NGGLQPAFAIFSKIGVTRIDDPETKQNSLFLALGIISPTFFLQGFPGA 780
DB 721 NGGLQPAFAIFSKIGVTRIDDPETKQNSLFLALGIISPTFFLQGFPGA 780
QY 781 GEILTKRLRYMVRMLQDVSWFDDPKNTTCALTRLANDAAQVKGAGSLAIIQNI 840
DB 781 GEILTKRLRYMVRMLQDVSWFDDPKNTTCALTRLANDAAQVKGAGSLAIIQNI 840
QY 841 ANLGTGIIISYIYQWLTLLAIIAIVPIIAIAGVVMKMLSGQALKDKKLEGGAGKATEA 900

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Db      841  ANLGTTGIIISFYGWQLTLLLAIVPIIAIAGVVMKQLSGQALDKKKELEGAKIATEA  900
Qy      901  IENFRTVVSUTQEQKPEHMYDOSLOVYRNSLRKAHIFGTFSTQAMMYFSVAGCFRFG  960
Db      901  IENFRTVVSUTQEQKPEHMYDOSLOVYRNSLRKAHIFGTFSTQAMMYFSVAGCFRFG  960
Qy      961  AYLVAHSLMSFEDVLLVFSVAVFGAMAVGVSSPAPYAKAKVSAHHIMIEKTPILDS  1020
Db      961  AYLVAHSLMSFEDVLLVFSVAVFGAMAVGVSSPAPYAKAKVSAHHIMIEKTPILDS  1020
Qy     1021  YSTEGKLPNTLEGNVTNEVFNYPTRLDIPVQLGSLVKKGQTLALVSSGCGKSTVV  1080
Db     1021  YSTEGKLPNTLEGNVTNEVFNYPTRLDIPVQLGSLVKKGQTLALVSSGCGKSTVV  1080
Qy     1081  QLLERFYDPLAGKVLDDGKEIKOLNQLVWLAHGIQVSOEPIIFDCSIAENIAYGDSRVV  1140
Db     1081  QLLERFYDPLAGKVLDDGKEIKOLNQLVWLAHGIQVSOEPIIFDCSIAENIAYGDSRVV  1140
Qy     1141  SOBEIVRAAKEANIHAFIESLPNKYSTKVGDKGTQLSGGQKQRIAIARALVRPHILLD  1200
Db     1141  SOBEIVRAAKEANIHAFIESLPNKYSTKVGDKGTQLSGGQKQRIAIARALVRPHILLD  1200
Qy     1201  EATSALDTESEKVVQVQALDKAREGRTCVIAHRLSTIQNALDLIVVFONGRVKEHGHQOL  1260
Db     1201  EATSALDTESEKVVQVQALDKAREGRTCVIAHRLSTIQNALDLIVVFONGRVKEHGHQOL  1260
Qy     1261  LAOKGIYFSMVSVQAGAKRQ  1280
Db     1261  LAOKGIYFSMVSVQAGAKRQ  1280

RESULT 14
5206352-4
; Patent No. 5206352
; Applicant: Robinson, Igor B.; Pastan Ira H.; Gottesman,
; Michael M.
; TITLE OF INVENTION: COMPOSITIONS FOR CLONES CONTAINING DNA
; SEQUENCES ASSOCIATED WITH MULTIDRUG RESISTANCE IN HUMAN CELLS
; NUMBER OF SEQUENCES: 4
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/622,836
; FILING DATE: 24-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 892,575
; FILING DATE: 01-AUG-1986
; APPLICATION NUMBER: 845,610
; FILING DATE: 28-MAR-1986
; SEQ ID NO: 4
; LENGTH: 1280
5206352-4

Query Match      96.6%; Score 6206; DB 7; Length 1280;
Best Local Similarity 96.5%; Pred. No. 0;
Matches 1235; Conservative 20; Mismatches 25; Indels 0; Gaps 0;

Qy      1  MDLEGGDRGAEKKNFFKLNKSKKKERKPTVSVFSMFYSNWLKLYVMVGTAAII  60
Db      1  MDLEGGDRGAEKKNFFKLNKSKKKERKPTVSVFSMFYSNWLKLYVMVGTAAII  60
Qy     61  HGAGLPLMLVFGDMTDTFANAGNLGDLGALLTNSNITDTPVPMNLFEEDMTRVAYYSG  120
Db     61  HGAGLPLMLVFGDMTDTFANAGNLGDLGALLTNSNITDTPVPMNLFEEDMTRVAYYSG  120
Qy     121  IGAGVLAAYIQVSWFCLAAQRQTHKIRKQPFHMRQEIQWFDVHVGELNLTDDVS  180
Db     121  IGAGVLAAYIQVSWFCLAAQRQTHKIRKQPFHMRQEIQWFDVHVGELNLTDDVS  180
Qy     181  KINGIGDKIMFTQSNATFTFGIVGTRGWKLTVLILASPVLGSAAWAKILSSFT  240
Db     181  KINGIGDKIMFTQSNATFTFGIVGTRGWKLTVLILASPVLGSAAWAKILSSFT  240
Qy     241  DKELLAYAKAGAAEVLAAIRTVIAFGQKKELERYNNKLEAKRIGIKKAITANISIG  300

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QY 1 MDLEGRNGAEGKKNFFKLNKSKDKKPKPTVSFPMFYSNWLKLYVVGTLAAII 60
DB 1 MDLEGRNGAEGKKNFFKLNKSKDKKPKPTVSFPMFYSNWLKLYVVGTLAAII 60
QY 61 HGAGLPLMLVFGDMTDTFANAGNLGDLGALL--TNSNITDTVPVNLLEEDMTRVAY 117
DB 61 HGAGLPLMLVFGDMTDTFANAGNLGDLGALLFNNTNSNITDTVPVNLLEEDMTRVAY 120
QY 118 YSGIGAGLVAAIYQVSFWCLAAAGROHKKIRKQFHAIHQEIGWFDVHVDGELNRLTD 177
DB 121 YSGIGAGLVAAIYQVSFWCLAAAGROHKKIRKQFHAIHQEIGWFDVHVDGELNRLTD 180
QY 178 DYSKINEGIDKLGMPFQSMATFTGFIQVFTGKWLTLVILAIQVGLSAVAWAKILS 237
DB 181 DYSKINEGIDKLGMPFQSMATFTGFIQVFTGKWLTLVILAIQVGLSAVAWAKILS 240
QY 238 SFTDKELLAYAKAGAAVEVLAAIRTVIAFGGOKKELERNYNKLEAKRIGIKKAITANI 297
DB 241 SFTDKELLAYAKAGAAVEVLAAIRTVIAFGGOKKELERNYNKLEAKRIGIKKAITANI 300
QY 298 SIGAAFLIIYASVALAFWYGTTLVLKSEYSGVLTVPFVSVLIGAFVGOASPSIERAFAN 357
DB 301 SIGAAFLIIYASVALAFWYGTTLVLKSEYSGVLTVPFVSVLIGAFVGOASPSIERAFAN 360
QY 358 ARGAAPFIIKIDNKPSIDYSKSGHKPDNIKGNLERNVHFSPSRKEVKILKGLNKKV 417
DB 361 ARGAAPFIIKIDNKPSIDYSKSGHKPDNIKGNLERNVHFSPSRKEVKILKGLNKKV 420
QY 418 QSGTVALVNGSGCGKSTTVLMQRLYDPTGEMVSDGQDIRTNVFLREIIGVVSQEP 477
DB 421 QSGTVALVNGSGCGKSTTVLMQRLYDPTGEMVSDGQDIRTNVFLREIIGVVSQEP 480
QY 478 VLFATTIAENIRYGREVDVTMDELEKAYKEANAYDFIMKLPQKFDTLVGERGAQSGGQK 537
DB 481 VLFATTIAENIRYGREVDVTMDELEKAYKEANAYDFIMKLPQKFDTLVGERGAQSGGQK 540
QY 538 RIAIARALVRNPKILLDEATSAIDTSEAVVQVALDKARKGRTTIVIAHRLSTVRNADV 597
DB 541 RIAIARALVRNPKILLDEATSAIDTSEAVVQVALDKARKGRTTIVIAHRLSTVRNADV 600
QY 598 IAGFDGVIYKGNHDELMKEGIIYFKLVMTQTAGNIELENADESKSIDTLEMSHD 657
DB 601 IAGFDGVIYKGNHDELMKEGIIYFKLVMTQTAGNIELENADESKSIDTLEMSHD 660
QY 658 SGSSLRKRSTRSVRSGQDRKLSYKEALDESIPVPSFWRIMKLNLTWPYFVVGVC 717
DB 661 SGSSLRKRSTRSVRSGQDRKLSYKEALDESIPVPSFWRIMKLNLTWPYFVVGVC 720
QY 718 AITNGLOPAPAVIFSIIIGITRNDDAETKRONSLFSLFLVLGIVSFTTFLQGTFF 777
DB 721 AITNGLOPAPAVIFSIIIGITRNDDAETKRONSLFSLFLVLGIVSFTTFLQGTFF 780
QY 778 GKAGEITLTKELRYVWFMSLRQDVSWFDDPKNTGTALTTRLANDAAOVKGAISRLAIT 837
DB 781 GKAGEITLTKELRYVWFMSLRQDVSWFDDPKNTGTALTTRLANDAAOVKGAISRLAIT 840
QY 838 QNTANLGTGIIISLIYQWQLTLALLAIVPIIAGVVMKLSQALDKKKELEGACKIA 897
DB 841 QNTANLGTGIIISLIYQWQLTLALLAIVPIIAGVVMKLSQALDKKKELEGACKIA 900
QY 898 TEAIENRPTVSTLTOEQKPEHMYDQSLQVPRNSLRKAHIFGITFTSQAMTFYSYAGCP 957
DB 901 TEAIENRPTVSTLTOEQKPEHMYDQSLQVPRNSLRKAHIFGITFTSQAMTFYSYAGCF 960
QY 958 RFCAYLVAHSLMFEDVLLVPSAVVFCAMAVQVSSFPADYAKAKVSAAHIMIEKTPL 1017
DB 961 RFCAYLVAHSLMFEDVLLVPSAVVFCAMAVQVSSFPADYAKAKVSAAHIMIEKTPL 1020
QY 1018 IDSYSTGLKPNLTLEGNVTNEVFNPTPLDIPVLQGLSLKVKKGOTLALVSSGCGKS 1077
DB 1021 IDSYSTGLKPNLTLEGNVTNEVFNPTPLDIPVLQGLSLKVKKGOTLALVSSGCGKS 1080
QY 1078 TVVQLLRFYDPLAGKVLDDGKEIKQLNVQWLAHGLGVQSEPIFLDCSISENIAVGDNS 1137

DB 1081 TVVQLLRFYDPLAGKVLDDGKEIKQLNVQWLAHGLGVQSEPIFLDCSISENIAVGDNS 1140
QY 1138 RVVQSEIVRAAKEANIHAIESLPLNKYSTRVGDGKTQSGGOKQRIARALVRPHIL 1197
DB 1141 RVVQSEIVRAAKEANIHAIESLPLNKYSTRVGDGKTQSGGOKQRIARALVRPHIL 1200
QY 1198 LIDEATSALDTESEKVVQVQALDKAREGRTCIIVIAHRLSTIQNALDLIVVQNGRVKHEGTH 1257
DB 1201 LIDEATSALDTESEKVVQVQALDKAREGRTCIIVIAHRLSTIQNALDLIVVQNGRVKHEGTH 1260
QY 1258 QQLLAOKGIYFVSVMVSVQAGAKRQ 1280
DB 1261 QQLLAOKGIYFVSVMVSVQAGAKRQ 1283

RESULT 6

US-09-584-586-2

Sequence 2, Application US/09584586

Patent No. 6933130

GENERAL INFORMATION:

APPLICANT: Sorrentino, Brian

APPLICANT: Bunting, Kevin

TITLE OF INVENTION: EXPANSION OF HEMATOPOIETIC STEM CELLS TRANSDUCED WITH

TITLE OF INVENTION: MDR-1 METHODS OF USE THEREOF

FILE REFERENCE: 1340-1-021CIP

CURRENT APPLICATION NUMBER: US/09/584,586

CURRENT FILING DATE: 2000-05-31

EARLIER APPLICATION NUMBER: US 60/086,988

EARLIER FILING DATE: 1998-05-28

EARLIER APPLICATION NUMBER: PCT/US99/11825

EARLIER FILING DATE: 1999-05-27

NUMBER OF SEQ ID NOS: 16

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 2

LENGTH: 1280

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: Human MDR 185-G

US-09-584-586-2

Query Match

Best Local Similarity 96.8%; Score 6218; DB 2; Length 1280;

Matches 1237; Conservative 19; Mismatches 24; Indels 0; Gaps 0;

QY 1 MDLEGRNGAEGKKNFFKLNKSKDKKPKPTVSFPMFYSNWLKLYVVGTLAAII 60
DB 1 MDLEGRNGAEGKKNFFKLNKSKDKKPKPTVSFPMFYSNWLKLYVVGTLAAII 60
QY 61 HGAGLPLMLVFGDMTDTFANAGNLGDLGALLFNNTNSNITDTVPVNLLEEDMTRVAY 120
DB 61 HGAGLPLMLVFGDMTDTFANAGNLGDLGALLFNNTNSNITDTVPVNLLEEDMTRVAY 120
QY 121 IGAGLVAAIYQVSFWCLAAAGROHKKIRKQFHAIHQEIGWFDVHVDGELNRLTDVVS 180
DB 121 IGAGLVAAIYQVSFWCLAAAGROHKKIRKQFHAIHQEIGWFDVHVDGELNRLTDVVS 180
QY 181 KINEGIDKLGMPFQSMATFTGFIQVFTGKWLTLVILAIQVGLSAVAWAKILSSFT 240
DB 181 KINEGIDKLGMPFQSMATFTGFIQVFTGKWLTLVILAIQVGLSAVAWAKILSSFT 240
QY 241 DKELLAYAKAGAAVEVLAAIRTVIAFGGOKKELERNYNKLEAKRIGIKKAITANISIG 300
DB 241 DKELLAYAKAGAAVEVLAAIRTVIAFGGOKKELERNYNKLEAKRIGIKKAITANISIG 300
QY 301 AAPLLIYASVALAFWYGTTLVLKSEYSGVLTVPFVSVLIGAFVGOASPSIERAFANARG 360
DB 301 AAPLLIYASVALAFWYGTTLVLKSEYSGVLTVPFVSVLIGAFVGOASPSIERAFANARG 360
QY 361 AAPFEIKIDNKPSIDYSKSGHKPDNIKGNLERNVHFSPSRKEVKILKGLNKLKQVSG 420
DB 361 AAPFEIKIDNKPSIDYSKSGHKPDNIKGNLERNVHFSPSRKEVKILKGLNKLKQVSG 420


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QY 421 QTVALVNSGCGKSTTVLMORLYDPTGEMVSDGQDRTINVRFLREIIGVVSQBPVLF 480
DB 421 QTVALVNSGCGKSTTVLMORLYDPTGEMVSDGQDRTINVRFLREIIGVVSQBPVLF 480
QY 481 ATTIAENIRYGRNVTMDIEKAVKEANAYDFIMKLPQKFDTLVGERGAQLSGGQKORIA 540
DB 481 ATTIAENIRYGRNVTMDIEKAVKEANAYDFIMKLPQKFDTLVGERGAQLSGGQKORIA 540
QY 541 IARALVRNPKILLDEATSALETSALDTESEAVVOVALDKARKGRTTIVIAHRLSTVRNADVIAG 600
DB 541 IARALVRNPKILLDEATSALETSALDTESEAVVOVALDKARKGRTTIVIAHRLSTVRNADVIAG 600
QY 601 FDDGVIVKGNHDELMKEGIYFKLVMTQTAGNEIELENAADESKSEIDTLEMSSDSS 660
DB 601 FDDGVIVKGNHDELMKEGIYFKLVMTQTAGNEIELENAADESKSEIDTLEMSSDSS 660
QY 661 SLIRKSTRSRVSGSQODRKLTSTKEALDESIPPSFWRMKLNLTENWPFVVGVCALII 720
DB 661 SLIRKSTRSRVSGSQODRKLTSTKEALDESIPPSFWRMKLNLTENWPFVVGVCALII 720
QY 721 NGGLQAPAFVIFSKIIIGVTRNDADPTKQNSNLSLFLVLGIVSFTFFLQGFPGKA 780
DB 721 NGGLQAPAFVIFSKIIIGVTRNDADPTKQNSNLSLFLVLGIVSFTFFLQGFPGKA 780
QY 781 GEILTKRLRYMYFRSMRLQDVSWFDDPKNTTGALTTRLANDAAOVKGAIGSLAIITONI 840
DB 781 GEILTKRLRYMYFRSMRLQDVSWFDDPKNTTGALTTRLANDAAOVKGAIGSLAIITONI 840
QY 841 ANLGTGIIISLYGQWLTLLMLAIVPIIAIAGVEMKMLSGQALDKKKELEGAGKIATEA 900
DB 841 ANLGTGIIISLYGQWLTLLMLAIVPIIAIAGVEMKMLSGQALDKKKELEGAGKIATEA 900
QY 901 IENFTVSVLTQEQFHEMYDOSLOVPYRNSLRKAHIFGITPSFTQAMMYFSYACGFRFG 960
DB 901 IENFTVSVLTQEQFHEMYDOSLOVPYRNSLRKAHIFGITPSFTQAMMYFSYACGFRFG 960
QY 961 AYLVASHLSMEDVLLVFSNAVFGAMAVGVSSPAPDYAKAKVSAHAHIMIEKTPILDS 1020
DB 961 AYLVASHLSMEDVLLVFSNAVFGAMAVGVSSPAPDYAKAKVSAHAHIMIEKTPILDS 1020
QY 1021 YSTGLKENTLEGNTFNWENFYPTRLDIPVLQGLSLEVKGGQTLALVSGSGCKSTV 1080
DB 1021 YSTGLKENTLEGNTFNWENFYPTRLDIPVLQGLSLEVKGGQTLALVSGSGCKSTV 1080
QY 1081 QLLERFYDPLAGKVLDDGKEIKQLNVQMLRAHLGIVSQEPILFDCSISENTAYGNSRV 1140
DB 1081 QLLERFYDPLAGKVLDDGKEIKQLNVQMLRAHLGIVSQEPILFDCSISENTAYGNSRV 1140
QY 1141 SQEETVRAAKENIHAFTESLPNKYSTVKGDKTOLSGGQKORIAIARALVRQPHILLD 1200
DB 1141 SQEETVRAAKENIHAFTESLPNKYSTVKGDKTOLSGGQKORIAIARALVRQPHILLD 1200
QY 1201 EATSALDTESEKVOEALDKAREGRTICIVIAHRLSTIONADLIIVFQNGRVRKEHGHQOL 1260
DB 1201 EATSALDTESEKVOEALDKAREGRTICIVIAHRLSTIONADLIIVFQNGRVRKEHGHQOL 1260
QY 1261 LAQKGIYFSMVSVQAGKRRQ 1280
DB 1261 LAQKGIYFSMVSVQAGKRRQ 1280
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RESULT 7

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US-09-767-594-2
; Sequence 2, Application US/09767594
; Patent No. 6521635
; GENERAL INFORMATION:
; APPLICANT: Bates, Susan
; APPLICANT: Robey, Robert
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Inhibition of MXR Transport by Acridine Derivatives
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; FILE REFERENCE: 015280-402100US
; CURRENT APPLICATION NUMBER: US/09/767,594
; CURRENT FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: US 60/177,410
; PRIOR FILING DATE: 2000-01-20
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1280
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human P-glycoprotein (Pgp)/multi-drug resistance 1
; OTHER INFORMATION: (Mdr-1) ATP-binding cassette (ABC transporter)
; OTHER INFORMATION: protein
; US-09-767-594-2
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Query Match 96.6%; Score 6209; DB 2; Length 1280;
Best Local Similarity 96.6%; Pred. No. 0;
Matches 1236; Conservative 19; Mismatches 25; Indels 0; Gaps 0;

QY 1 MDLEGRNGCAEKKNFKLNKSKDKKERKPTVSVFSPRYSNWLDKLYMVVGTLLAII 60
DB 1 MDLEGRNGCAEKKNFKLNKSKDKKERKPTVSVFSPRYSNWLDKLYMVVGTLLAII 60
QY 61 HGAGLPLMLVFGDMTDTTFANAGNLGDLGALLTNSNITDTVPVNNLEEDMTRYAYYS 120
DB 61 HGAGLPLMLVFGDMTDTTFANAGNLGDLGALLTNSNITDTVPVNNLEEDMTRYAYYS 120
QY 121 IGAGVLAAYIQVSPWCLAAAGROHKIRKQFFHAIHQEIGWFDVHVGELNLTDDVS 180
DB 121 IGAGVLAAYIQVSPWCLAAAGROHKIRKQFFHAIHQEIGWFDVHVGELNLTDDVS 180
QY 181 KINEGIGDKIMGFQSMATFTGTVGTRGWLTLVLALSPVLGLSAAVWAKILSFT 240
DB 181 KINEGIGDKIMGFQSMATFTGTVGTRGWLTLVLALSPVLGLSAAVWAKILSFT 240
QY 241 DKELLAYAKGAVAEVLAARITVIAFGGQKELERYNNKLEAKRIGIKAITANISIG 300
DB 241 DKELLAYAKGAVAEVLAARITVIAFGGQKELERYNNKLEAKRIGIKAITANISIG 300
QY 301 AAFLLIYASVALAPWYGTTLVLSKEYSIGVLTVPFESVLICAPSVGOASPIERANARG 360
DB 301 AAFLLIYASVALAPWYGTTLVLSKEYSIGVLTVPFESVLICAPSVGOASPIERANARG 360
QY 361 AAFEIFKIIDNKPSIDSYSGSKHKNKGNLFRNVHFSYPSRKEVKILKGLNKLKVSQ 420
DB 361 AAFEIFKIIDNKPSIDSYSGSKHKNKGNLFRNVHFSYPSRKEVKILKGLNKLKVSQ 420
QY 421 QTVALVNSGCGKSTTVLMORLYDPTGEMVSDGQDRTINVRFLREIIGVVSQBPVLF 480
DB 421 QTVALVNSGCGKSTTVLMORLYDPTGEMVSDGQDRTINVRFLREIIGVVSQBPVLF 480
QY 481 ATTIAENIRYGRNVTMDIEKAVKEANAYDFIMKLPQKFDTLVGERGAQLSGGQKORIA 540
DB 481 ATTIAENIRYGRNVTMDIEKAVKEANAYDFIMKLPQKFDTLVGERGAQLSGGQKORIA 540
QY 541 IARALVRNPKILLDEATSALETSALDTESEAVVOVALDKARKGRTTIVIAHRLSTVRNADVIAG 600
DB 541 IARALVRNPKILLDEATSALETSALDTESEAVVOVALDKARKGRTTIVIAHRLSTVRNADVIAG 600
QY 601 FDDGVIVKGNHDELMKEGIYFKLVMTQTAGNEIELENAADESKSEIDTLEMSSDSS 660
DB 601 FDDGVIVKGNHDELMKEGIYFKLVMTQTAGNEIELENAADESKSEIDTLEMSSDSS 660
QY 661 SLIRKSTRSRVSGSQODRKLTSTKEALDESIPPSFWRMKLNLTENWPFVVGVCALII 720
DB 661 SLIRKSTRSRVSGSQODRKLTSTKEALDESIPPSFWRMKLNLTENWPFVVGVCALII 720
QY 721 NGGLQAPAFVIFSKIIIGVTRNDADPTKQNSNLSLFLVLGIVSFTFFLQGFPGKA 780
DB 721 NGGLQAPAFVIFSKIIIGVTRNDADPTKQNSNLSLFLVLGIVSFTFFLQGFPGKA 780
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QY 1141 SOEIVRAAKANIHAFIESLPNKYSTKVGDKGTOLSGQKQRIAAIALVROPHILLD 1200
Db 1141 SOEIVRAAKANIHAFIESLPNKYSTKVGDKGTOLSGQKQRIAAIALVROPHILLD 1200
QY 1201 EATSALDTESEKVVQVQALDKAREGTCIVIAHRLSTIQNADLI VVFQNGRVEHGTQOOL 1260
Db 1201 EATSALDTESEKVVQVQALDKAREGTCIVIAHRLSTIQNADLI VVFQNGRVEHGTQOOL 1260
QY 1261 LAQGIYFSMVSVQAGTKRQ 1280
Db 1261 LAQGIYFSMVSVQAGTKRQ 1280

RESULT 4
US-10-101-433A-5
; Sequence 5, Application US/10101433A
; Patent No. 685812
; GENERAL INFORMATION:
; APPLICANT: Hanscom, Sara
; APPLICANT: Crepi, Charles
; TITLE OF INVENTION: P-GLYCOPROTEINS AND USES THEREOF
; FILE REFERENCE: G00307/70019
; CURRENT APPLICATION NUMBER: US/10/101,433A
; PRIOR FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: US 60/277,095
; PRIOR FILING DATE: 2001-03-19
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 5
; LENGTH: 1280
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-101-433A-5

Query Match 100.0%; Score 6431; DB 2; Length 1280;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDLEGRNGAKKNNFKLNKSEKDKKKPTVSVFSPRYSNWLDKLYMVGTAAII 60
Db 1 MDLEGRNGAKKNNFKLNKSEKDKKKPTVSVFSPRYSNWLDKLYMVGTAAII 60
QY 61 HGAGLPLMVLCEMTDIFANAGNLEDLMSNITNRSNDINTGFFNLEEDMTYAYYS 120
Db 61 HGAGLPLMVLCEMTDIFANAGNLEDLMSNITNRSNDINTGFFNLEEDMTYAYYS 120
QY 121 IGAGVLVAAYIOVSFWCLAGRQIHKIRKOPFHAINRQIGWFDHVGELNRLTDDVS 180
Db 121 IGAGVLVAAYIOVSFWCLAGRQIHKIRKOPFHAINRQIGWFDHVGELNRLTDDVS 180
QY 181 KINEVIGDKIGMFFOSMATFTFTGIVGTRGKLTILAILSPVLGLSNAVWAKILSFT 240
Db 181 KINEVIGDKIGMFFOSMATFTFTGIVGTRGKLTILAILSPVLGLSNAVWAKILSFT 240
QY 241 DKELLAYAKAGAAEVLAAITRTVAFGGQKELERYNKNLEAKRIGIKKAITANISIG 300
Db 241 DKELLAYAKAGAAEVLAAITRTVAFGGQKELERYNKNLEAKRIGIKKAITANISIG 300
QY 301 AAFLLIYASALAFWYGTTLVLSEYSIGQVLTFFSVLIGAFVQASPSIEAFANARG 360
Db 301 AAFLLIYASALAFWYGTTLVLSEYSIGQVLTFFSVLIGAFVQASPSIEAFANARG 360
QY 361 AAYEIFIKIDNKPSIDSYSGSHKPDNIKGNLEPRNVHESVPSRKEVKILKGLNKLKVSQ 420
Db 361 AAYEIFIKIDNKPSIDSYSGSHKPDNIKGNLEPRNVHESVPSRKEVKILKGLNKLKVSQ 420
QY 421 QTVLVGNSCGSSTTVLMQRLYDPTGEMVSDGDIRTINVRFLREIIGVVSQBPVL 480
Db 421 QTVLVGNSCGSSTTVLMQRLYDPTGEMVSDGDIRTINVRFLREIIGVVSQBPVL 480
QY 481 ATTIAENIRYGRNVMTDEIEKAVKEANAYDFIMKLPKFDTLVGERGAOLSGQKQRIA 540
Db 481 ATTIAENIRYGRNVMTDEIEKAVKEANAYDFIMKLPKFDTLVGERGAOLSGQKQRIA 540

RESULT 5
US-09-817-762-3
; Sequence 3, Application US/09817762
; Patent No. 6858774
; GENERAL INFORMATION:
; APPLICANT: Spalding, Edgar P.
; APPLICANT: No. 6858774, Bosl
; TITLE OF INVENTION: MDR-Like ABC Transporter Gene From
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 13238-00061
; CURRENT APPLICATION NUMBER: US/09/817,762
; CURRENT FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: PCT/US99/22363
; PRIOR FILING DATE: 1999-09-24
; PRIOR APPLICATION NUMBER: US 60/101,814
; PRIOR FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0

Db 481 ATTIAENIRYGRNVMTDEIEKAVKEANAYDFIMKLPKFDTLVGERGAOLSGQKQRIA 540
QY 541 IARALVRNPKILLDEATSALDTESEAVVQVQALDKARKGRTTIVIAHRLSTVRNADVIAG 600
Db 541 IARALVRNPKILLDEATSALDTESEAVVQVQALDKARKGRTTIVIAHRLSTVRNADVIAG 600
QY 601 FDCGVIVKGNHDELAKKEGIYFKLVTMOTAGNEVELENAADESKSEIDALENSSNDSRS 660
Db 601 FDCGVIVKGNHDELAKKEGIYFKLVTMOTAGNEVELENAADESKSEIDALENSSNDSRS 660
QY 661 SLIRKSTRSVRGSAQDRKLTKEALDESI PPVSWFKIMKLNLTENWFFVVGVCALII 720
Db 661 SLIRKSTRSVRGSAQDRKLTKEALDESI PPVSWFKIMKLNLTENWFFVVGVCALII 720
QY 721 NGLOPAPAFIIFSKIIGVFTTRIDDPETKRONSLFSLFALGIIISFIFFLQGGTFGKA 780
Db 721 NGLOPAPAFIIFSKIIGVFTTRIDDPETKRONSLFSLFALGIIISFIFFLQGGTFGKA 780
QY 781 GEILTCLRVRNMFVRSMLRQDVSWFDDPKNTTGALTTRLANDAAQVKGAGISRLAVITQNI 840
Db 781 GEILTCLRVRNMFVRSMLRQDVSWFDDPKNTTGALTTRLANDAAQVKGAGISRLAVITQNI 840
QY 841 ANLGTGIIISFIYQWLTLLAILAIVPIIAIAGVVMKMLSGOALKDKKELEGAGKIATEA 900
Db 841 ANLGTGIIISFIYQWLTLLAILAIVPIIAIAGVVMKMLSGOALKDKKELEGAGKIATEA 900
QY 901 IENPRTVVSITOBQKFEHMYAQSLQVPRNSLRKAHIFGITFTFOAMMYFVAGCFRFG 960
Db 901 IENPRTVVSITOBQKFEHMYAQSLQVPRNSLRKAHIFGITFTFOAMMYFVAGCFRFG 960
QY 961 AYLVAHKLMSFEDVLLVFSVAVFGMAVGOVSPADYAKAKISAAHIMIIEKTEPLIDS 1020
Db 961 AYLVAHKLMSFEDVLLVFSVAVFGMAVGOVSPADYAKAKISAAHIMIIEKTEPLIDS 1020
QY 1021 YSTEGMPNTLEGNVTFGEVFNYPTRPDI PVQLGLELVKGGOTLALVSSGCGKSTVV 1080
Db 1021 YSTEGMPNTLEGNVTFGEVFNYPTRPDI PVQLGLELVKGGOTLALVSSGCGKSTVV 1080
QY 1081 QLLERYDPLACKVLLDGKEIKRLNVQMLRAHGLIVSQEPILFDCSIAENIAYGNSRVV 1140
Db 1081 QLLERYDPLACKVLLDGKEIKRLNVQMLRAHGLIVSQEPILFDCSIAENIAYGNSRVV 1140
QY 1141 SOEIVRAAKANIHAFIESLPNKYSTKVGDKGTOLSGQKQRIAAIALVROPHILLD 1200
Db 1141 SOEIVRAAKANIHAFIESLPNKYSTKVGDKGTOLSGQKQRIAAIALVROPHILLD 1200
QY 1201 EATSALDTESEKVVQVQALDKAREGTCIVIAHRLSTIQNADLI VVFQNGRVEHGTQOOL 1260
Db 1201 EATSALDTESEKVVQVQALDKAREGTCIVIAHRLSTIQNADLI VVFQNGRVEHGTQOOL 1260
QY 1261 LAQGIYFSMVSVQAGTKRQ 1280
Db 1261 LAQGIYFSMVSVQAGTKRQ 1280

Qy	901	1ENFRTVVSLSLTOEQKFHEHMYAQSLOQVPRNSLRKAHIFGITFTSQAMVFSYAGCPRFG	960
Db	901	1ENFRTVVSLSLTOEQKFHEHMYAQSLOQVPRNSLRKAHIFGITFTSQAMVFSYAGCPRFG	960
Qy	961	AYLVAHKLMSFEDVLLVFSAVVFCGAMVGVSSFPADPYAKAKISAHHIMIEKTPILDS	1020
Db	961	AYLVAHKLMSFEDVLLVFSAVVFCGAMVGVSSFPADPYAKAKISAHHIMIEKTPILDS	1020
Qy	1021	YSTBGLMPNTLEGNVTFGEVFNFTPRDIPVLQGLSLEVKKGOTLALVGSSGCGKSTVV	1080
Db	1021	YSTBGLMPNTLEGNVTFGEVFNFTPRDIPVLQGLSLEVKKGOTLALVGSSGCGKSTVV	1080
Qy	1081	QLLERFYDPLAGKVLLDGKEIKRLNVOWLRAHLGIVSQEPIFDCAENIAYGDNRSRV	1140
Db	1081	QLLERFYDPLAGKVLLDGKEIKRLNVOWLRAHLGIVSQEPIFDCAENIAYGDNRSRV	1140
Qy	1141	SOEIVRAAKEANIHAIESLPNKYSTKVGDKGTOLSGGOKRIATARALVROPHILLD	1200
Db	1141	SOEIVRAAKEANIHAIESLPNKYSTKVGDKGTOLSGGOKRIATARALVROPHILLD	1200
Qy	1201	EATSALDTESEKVVQOEALDKAREGRTCIVIAHRLSTIQNADLI VVFONGRVKEHGTQOOL	1260
Db	1201	EATSALDTESEKVVQOEALDKAREGRTCIVIAHRLSTIQNADLI VVFONGRVKEHGTQOOL	1260
Qy	1261	LAQKGIYFSMVSVQAGTKRQ	1280
Db	1261	LAQKGIYFSMVSVQAGTKRQ	1280

RESULT 6
US-09-584-586-4
; Sequence 4, Application US/09584586
; Patent No. 6933150
; GENERAL INFORMATION:
; APPLICANT: Bunting, Kevin
; TITLE OF INVENTION: EXPANSION OF HEMATOPOIETIC STEM CELLS TRANSDUCED WITH
; FILE OF INVENTION: MDR-1 METHODS OF USE THEREOF
; FILE REFERENCE: 1340-1-021CIP
; CURRENT APPLICATION NUMBER: US/09/584,586
; CURRENT FILING DATE: 2000-05-31
; EARLIER APPLICATION NUMBER: US 60/086,988
; EARLIER FILING DATE: 1998-05-28
; EARLIER APPLICATION NUMBER: PCT/US99/11825
; EARLIER FILING DATE: 1999-05-27
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 1280
; TYPE: PRN
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Human MDR 185-V
US-09-584-586-4

Query Match		100.0%;	Score 6431;	DB 2;	Length 1280;
Best Local Similarity		100.0%;	Pred. No. 0;		
Matches 1280;		Conservative	0;	Mismatches	0;
				Indels	0;
				Gaps	0;
Qy	1	MDLEGRNGGAKKKNFFKLNKSEKDKKXKPTVSVFSMFRYSNWLDKLYVWVGTLAAII	60		
Db	1	MDLEGRNGGAKKKNFFKLNKSEKDKKXKPTVSVFSMFRYSNWLDKLYVWVGTLAAII	60		
Qy	61	HGAGLPLMLVFGEMTDIFANAGNLEDLMSNITNRSNDINDTGFFMNLLEEDMTRYAYYSG	120		
Db	61	HGAGLPLMLVFGEMTDIFANAGNLEDLMSNITNRSNDINDTGFFMNLLEEDMTRYAYYSG	120		
Qy	121	IGAGLVAAIYQVSFWCLAGQIHKIRKOPFHAIMRQIHFEDVHDVGLNTRLTDDVS	180		
Db	121	IGAGLVAAIYQVSFWCLAGQIHKIRKOPFHAIMRQIHFEDVHDVGLNTRLTDDVS	180		
Qy	181	KINEVIGDKIGNPFOSMATFFTGFIYGFTRGWKLTLVILAISPVLGISA VVAKILSSFT	240		

Db 181 KINEVIGDKIGMFQSMATFTFTGTVGTRGKWLTLVLAISPVGLSAAVWAKILSSFT 240
Qy 241 DKELLAYAKAGAAVEVLAAITRTVAFGGOKKELRYNKNLEBAKRIKKAITANISIG 300
Db 241 DKELLAYAKAGAAVEVLAAITRTVAFGGOKKELRYNKNLEBAKRIKKAITANISIG 300
Qy 301 AAFLLIYASYALAFWYGTTLVLSGYSIGQVLTVPFVSVLIGAFSGVQASPSIEAFANARG 360
Db 301 AAFLLIYASYALAFWYGTTLVLSGYSIGQVLTVPFVSVLIGAFSGVQASPSIEAFANARG 360
Qy 361 AAAYEIKIIDNKPSIDSKSGHKPDNKGKLNFRNVHFSVPSRKEVKILKGLNLKVQSG 420
Db 361 AAAYEIKIIDNKPSIDSKSGHKPDNKGKLNFRNVHFSVPSRKEVKILKGLNLKVQSG 420
Qy 421 QTVALVNGSGGKSTTVQMLQRLYDPTGSMVSDQDRTINVRFLRIIIGVQEPVLF 480
Db 421 QTVALVNGSGGKSTTVQMLQRLYDPTGSMVSDQDRTINVRFLRIIIGVQEPVLF 480
Qy 481 ATTIAENIRYGRNVMTDEIEKAVKEANAYDFIMKLPKHFTDLVGERGAQLSGGQKRIA 540
Db 481 ATTIAENIRYGRNVMTDEIEKAVKEANAYDFIMKLPKHFTDLVGERGAQLSGGQKRIA 540
Qy 541 IARALVRNPKILLDEATSDALDTSEAVVQVALDKARKGRTTIVIAHRLSTVRNADVIAG 600
Db 541 IARALVRNPKILLDEATSDALDTSEAVVQVALDKARKGRTTIVIAHRLSTVRNADVIAG 600
Qy 601 FDDGVIVEKGNHDEMEKGIYFKLVTMTAGNEVELENADESKSEIDALEMSNDRS 660
Db 601 FDDGVIVEKGNHDEMEKGIYFKLVTMTAGNEVELENADESKSEIDALEMSNDRS 660
Qy 661 SLIRKSTRSRVRSQADRLKSTKEALDESIPVPSFWRIMKLNLTWPYVGVVFCALI 720
Db 661 SLIRKSTRSRVRSQADRLKSTKEALDESIPVPSFWRIMKLNLTWPYVGVVFCALI 720
Qy 721 NGLOPAFAIFSKIIGVTFIDDPETKRONSLFSLFLALGIIISFIPFLOQFTFGKA 780
Db 721 NGLOPAFAIFSKIIGVTFIDDPETKRONSLFSLFLALGIIISFIPFLOQFTFGKA 780
Qy 781 GEILTKELRYVFSMLRQDVSFDDPKNTTGALTTLANDAAQVKAIGSLRAVITONI 840
Db 781 GEILTKELRYVFSMLRQDVSFDDPKNTTGALTTLANDAAQVKAIGSLRAVITONI 840
Qy 841 ANLGTGIIISFIPYQWLTLLALLAIVPIIATAGVEMKMLSGQALKDKKELEGAGKIATEA 900
Db 841 ANLGTGIIISFIPYQWLTLLALLAIVPIIATAGVEMKMLSGQALKDKKELEGAGKIATEA 900
Qy 901 IENPRTVSVLTQOKFHEHMAQSLQVPRNSLRKAHIFGITFSPTQAMVFSYAGCPRFG 960
Db 901 IENPRTVSVLTQOKFHEHMAQSLQVPRNSLRKAHIFGITFSPTQAMVFSYAGCPRFG 960
Qy 961 AYLVAHKLMSPEDVLLVFSVAVFGAMAVGVSSPAPDYAKAKISAAHIMIIEKTPILDS 1020
Db 961 AYLVAHKLMSPEDVLLVFSVAVFGAMAVGVSSPAPDYAKAKISAAHIMIIEKTPILDS 1020
Qy 1021 YSTEGMLPNTLEGNTVGEVVFNYPTRPDIPLVQLGSLEVKKGOTLALVSGSGCGKSTVV 1080
Db 1021 YSTEGMLPNTLEGNTVGEVVFNYPTRPDIPLVQLGSLEVKKGOTLALVSGSGCGKSTVV 1080
Qy 1081 QLLERFYDPLAGKVLLDGKEIKRLNVQWLRHAHLGIVSQEPILFDCSIAENIAYGDNRRV 1140
Db 1081 QLLERFYDPLAGKVLLDGKEIKRLNVQWLRHAHLGIVSQEPILFDCSIAENIAYGDNRRV 1140
Qy 1141 SQEIIVRAAKEANHAIESLPNKYSTKVGDKGTOLSGGOKORIAIARALVROPHILLD 1200
Db 1141 SQEIIVRAAKEANHAIESLPNKYSTKVGDKGTOLSGGOKORIAIARALVROPHILLD 1200
Qy 1201 EATSALDTSEKVVQEAALDKAREGRTCIVIAHRLSTIQNADLIIVFONGRKEHGHQOL 1260
Db 1201 EATSALDTSEKVVQEAALDKAREGRTCIVIAHRLSTIQNADLIIVFONGRKEHGHQOL 1260
Qy 1261 LAQKGIYFSMVSVQAGTKRQ 1280
Db 1261 LAQKGIYFSMVSVQAGTKRQ 1280

RESULT 7
US-08-583-276-19
; Sequence 19, Application US/08583276
; Patent No. 5837536
; GENERAL INFORMATION:
; APPLICANT: McDonagh, Kevin T.
; APPLICANT: Nienhuis, Arthur
; APPLICANT: Tolstoshev, Paul
; TITLE OF INVENTION: IMPROVED EXPRESSION OF HUMAN
; TITLE OF INVENTION: MULTIDRUG RESISTANCE GENES AND IMPROVED
; TITLE OF INVENTION: SELECTION OF CELLS TRANSFECTED WITH SUCH GENES
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
; ADDRESSEE: Cecchi & Stewart
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: DW4.V2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/583,276
; FILING DATE: 05-JAN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/332,444
; FILING DATE: 31-OCT-1994
; APPLICATION NUMBER: 07/887,712
; FILING DATE: 22-MAY-1992
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1280 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: protein
US-08-583-276-19

Query Match 99.9%; Score 6428; DB 1; Length 1280;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1279; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MLEGDRNGGAKKGNFFKLNKSEKDKKPKTVSVFSMFRYSNWLDKLYMVVGTLLAAII 60
Db 1 MLEGDRNGGAKKGNFFKLNKSEKDKKPKTVSVFSMFRYSNWLDKLYMVVGTLLAAII 60
Qy 61 HGAGLPLMLVFGEMTDIFANAGNLEDMSNTNRSNDINDTGFNMLEDMDTRYAYYSG 120
Db 61 HGAGLPLMLVFGEMTDIFANAGNLEDMSNTNRSNDINDTGFNMLEDMDTRYAYYSG 120
Qy 121 IGAGVLVAAYIQVSWCLAAAGRIHKIRKQFHAIMRQEIHFWDVHDVCELNTRLTDDVS 180
Db 121 IGAGVLVAAYIQVSWCLAAAGRIHKIRKQFHAIMRQEIHFWDVHDVCELNTRLTDDVS 180
Qy 181 KINEVIGDKIGMFQSMATFTFTGTVGTRGKWLTLVLAISPVGLSAAVWAKILSSFT 240
Db 181 KINEVIGDKIGMFQSMATFTFTGTVGTRGKWLTLVLAISPVGLSAAVWAKILSSFT 240
Qy 241 DKELLAYAKAGAAVEVLAAITRTVAFGGOKKELRYNKNLEBAKRIKKAITANISIG 300
Db 241 DKELLAYAKAGAAVEVLAAITRTVAFGGOKKELRYNKNLEBAKRIKKAITANISIG 300
Qy 301 AAFLLIYASYALAFWYGTTLVLSGYSIGQVLTVPFVSVLIGAFSGVQASPSIEAFANARG 360
Db 301 AAFLLIYASYALAFWYGTTLVLSGYSIGQVLTVPFVSVLIGAFSGVQASPSIEAFANARG 360

Db 418 QSGQTVLVGNSGGCKSTTVQLMORLYDPTBEGSVSDGQDIRTINVRFLRIIGVVSQEP 477
Qy 481 VLPATTAAENIRYGRDVTMDIEIEKAVEANAYDFIMKLPKQFDTLVGERGAQLSGGQKQ 540
Db 478 VLPATTAAENIRYGRDVTMDIEIEKAVEANAYDFIMKLPKQFDTLVGERGAQLSGGQKQ 537
Qy 541 RIAIARALVRNPKILLDEATSDALDTESEAVVQVALDKARKGRTTIVIAHRLSTVRNADV 600
Db 538 RIAIARALVRNPKILLDEATSDALDTESEAVVQVALDKARKGRTTIVIAHRLSTVRNADV 597
Qy 601 IAGPDDGVIVKGNHDELMKEGTYFKLVMTQTAGNEIELENADESKSEIDTLEMSSH 660
Db 598 IAGPDDGVIVKGNHDELMKEGTYFKLVMTQTAGNEIELENADESKSEIDTLEMSSH 657
Qy 661 SGSSLIIRKSTRRSVRSGQDRKLSKTEALDESIPVPSFWIRIMKLNLTENPFYVGVFC 720
Db 658 SGSSLIIRKSTRRSVRSGQDRKLSKTEALDESIPVPSFWIRIMKLNLTENPFYVGVFC 717
Qy 721 AINGGLQAPAFVIFSKIIIGIFTRNDADAETKQNSLFLVGLGIVSFITFLQGPTF 780
Db 718 AINGGLQAPAFVIFSKIIIGIFTRNDADAETKQNSLFLVGLGIVSFITFLQGPTF 777
Qy 781 GKAGEILTCLRIVMFRSMLRQDVSFDDPKNTTGALTTRLANDAAQVKGAGSLAII 840
Db 778 GKAGEILTCLRIVMFRSMLRQDVSFDDPKNTTGALTTRLANDAAQVKGAGSLAII 837
Qy 841 QNIANLGTIIISLYGWLTLALLAIVPIIAAGVEMKMLSGQALKKKELEGAGKIA 900
Db 838 QNIANLGTIIISLYGWLTLALLAIVPIIAAGVEMKMLSGQALKKKELEGAGKIA 897
Qy 901 TEAIENFRTVVSLSLQEQKFEMHQSLQVPRNSLRKAHIFGTFSTFOAMWYFSYAGCF 960
Db 898 TEAIENFRTVVSLSLQEQKFEMHQSLQVPRNSLRKAHIFGTFSTFOAMWYFSYAGCF 957
Qy 961 RFGAYLVASHLMSFEDVLLVFSVAVFGAMVGVSSPAPDYAKAKVSAHIMIIEKTP 1020
Db 958 RFGAYLVASHLMSFEDVLLVFSVAVFGAMVGVSSPAPDYAKAKVSAHIMIIEKTP 1017
Qy 1021 IDSYSTELKENTLEGNVTNEVFNYPTRLDIPVLQGLSLEVKKGQTLALVSGSGCKS 1080
Db 1018 IDSYSTELKENTLEGNVTNEVFNYPTRLDIPVLQGLSLEVKKGQTLALVSGSGCKS 1077
Qy 1081 TVQLLERFYDPLAGKVLDDGKEIKQLNVQMLRAHLGIVSQEPILFDCSISENTAYGNS 1140
Db 1078 TVQLLERFYDPLAGKVLDDGKEIKQLNVQMLRAHLGIVSQEPILFDCSISENTAYGNS 1137
Qy 1141 RVVSOEIVRAAKZANIIHAFIESLPNKYSTRVGDKGTQISGGQKQRIAIARALVRQPHIL 1200
Db 1138 RVVSOEIVRAAKZANIIHAFIESLPNKYSTRVGDKGTQISGGQKQRIAIARALVRQPHIL 1197
Qy 1201 LLDEATSDALDTESEKVOEALDKAREGTCIVIAHRLSTIONADLIVVFQGRVKEHGT 1260
Db 1198 LLDEATSDALDTESEKVOEALDKAREGTCIVIAHRLSTIONADLIVVFQGRVKEHGT 1257
Qy 1261 QOLLAQKGIYFSMVSQVQAKRQ 1283
Db 1258 QOLLAQKGIYFSMVSQVQAKRQ 1280

RESULT 5

ID MD1 HUMAN STANDARD. PRT; 1280 AA.
AC P08183; Q12755; Q14872;
DT 01-NOV-1998, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1997, sequence version 2.
DT 07-MAR-2006, entry version 78.
DE Multidrug resistance protein 1 (P-glycoprotein 1) (CD243 antigen).
GN Name=ABCB1; Synonyms=MDR1, PGP1,
OS Homo sapiens (Human),
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
NCBI_TaxID=9606;

RP NUCLEOTIDE SEQUENCE [MRNA], AND VARIANT VAL-185.
RX MEDLINE=87028230; PubMed=2876781; DOI=10.1016/0092-8674(86)90595-7;
RA Chen C.-J., Chin J.B., Ueda K., Clark D.P., Pastan I., Gottesman M.M.,
RA Roninson I.B.;
RT "Internal duplication and homology with bacterial transport proteins
in the mdr1 (P-glycoprotein) gene from multidrug-resistant human
cells.";
RL Cell 47:381-389 (1986).
[2]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RX MEDLINE=90094448; PubMed=1967175;
RA Chen C.-J., Clark D.P., Ueda K., Pastan I., Gottesman M.M.,
RA Roninson I.B.;
RT "Genomic organization of the human multidrug resistance (MDR1) gene
and origin of P-glycoproteins.";
RL J. Biol. Chem. 265:506-514 (1990).
[3]
RP NUCLEOTIDE SEQUENCE [MRNA], AND VARIANT VAL-185.
RX MEDLINE=97190336; PubMed=9038218; DOI=10.1074/jbc.272.9.5413;
RA Chen G., Duran G.E., Steger K.A., Lacayo N.J., Jaffrezou J.P.,
RA Dumontet C., Sikic B.I.;
RT "Multidrug-resistant human sarcoma cells with a mutant P-glycoprotein,
altered phenotype, and resistance to cyclosporins.";
RL J. Biol. Chem. 272:5974-5982 (1997).
[4]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANTS LEU-17; ASP-21;
RX AS-400; LYS-566; VAL-836; ALA-1051; THR-1141 AND ILE-1251.
RA Livingston R.J., Rieder M.J., Rajkumar N., Downing T.K., Olson A.N.,
RA Nguyen C.P., Gildersleeve H., Cassidy C.M., Johnson E.J.,
RA Swanson J.E., McFarland I., Tool B., Park C., Nickerson D.A.;
RT "NTEHS-SNPs, environmental genome project, NIEHS ES15478, Department
of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu).";
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
[5]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=22737999; PubMed=12853948; DOI=10.1038/nature01782;
RA Hillier L.W., Fulton R.S., Fulton L.A., Graves T.A., Pepin K.H.,
RA Wagner-McPherson C., Layman D., Maas J., Jaeger S., Walker R.,
RA Wyllie K., Sekhon M., Becker M.C., O'Laughlin M.D., Schaller M.E.,
RA Fewell G.A., Delehaanty K.D., Miner T.L., Nash W.E., Cordes M., Du H.,
RA Sun H., Edwards J., Bradshaw-Cordum H., Ali J., Andrews S., Isak A.,
RA Vanbrunt A., Nguyen C., Du F., Lamar B., Courtney L., Kalicki J.,
RA Ozersky P., Bielicki L., Scott K., Holmes A., Harkins R., Harris A.,
RA Strong C.M., Hou S., Tomlinson C., Dauphin-Kohlberg S.,
RA Kozlovic-Reilly A., Leonard S., Rohlfing T., Rock S.M.,
RA Tin-Wellam A.-M., Abbott A., Minx P., Maupin R., Strowmatt C.,
RA Latreille P., Miller N., Johnson D., Murray J., Woessner J.P.,
RA Wendt M.C., Yang S.-P., Schultz B.R., Wallis J.W., Spieth J.,
RA Bieri T.A., Nelson J.O., Berkowicz N., Wohldmann P.E., Cook L.L.,
RA Hickenbotham M.T., Eldred J., Williams D., Bedell J.A., Mardis E.R.,
RA Clifton S.W., Chisoe S.L., Marra M.A., Raymond C., Haugen E.,
RA Gillett W., Zhou Y., James R., Phelps K., Iadamoto S., Bubbs K.,
RA Simms E., Levy R., Clendenning J., Kaul R., Kent W.J., Furey T.S.,
RA Baertsch R.A., Brent M.R., Keibler E., Flicker P., Bork P., Suyama M.,
RA Bailey J.A., Portnoy M.E., Torrents D., Chinwalla A.T., Gish W.R.,
RA Eddy S.R., McPherson J.D., Olson M.V., Eichler E.E., Green E.D.,
RA Waterston R.H., Wilson R.K.;
RT "The DNA sequence of human chromosome 7.";
RL Nature 424:157-164 (2003).
[6]
RP NUCLEOTIDE SEQUENCE OF 178-215 AND 800-856.
RX MEDLINE=90290529; PubMed=1972623;
RA Gekeler V., Weger S., Probst H.;
RT "mdr1P-glycoprotein gene segments analyzed from various human
leukemic cell lines exhibiting different multidrug resistance
profiles.";
RL Biochem. Biophys. Res. Commun. 169:796-802 (1990).
[7]
RP NUCLEOTIDE SEQUENCE OF 1-23, AND VARIANT SER-893.
RX MEDLINE=89322246; PubMed=2568932;
RA Kioka N., Tsubota J., Kakehi Y., Komano T., Gottesman M.M., Pastan I.,
RA Ueda K.;

358 ARGAAYEIPKIIDNKPISIDYSKSGHKPDNKGKLNLEFRNVHFSYPSRKEVKILKGLNLKV 417
421 QSGQTVALVNSCGSKSTTQVMQRLYDPTGEMVSDGQDRTINVEFLREIIGVWSQEP 480
418 QSGQTVALVNSCGSKSTTQVMQRLYDPTGEMVSDGQDRTINVEFLREIIGVWSQEP 477
481 VLPATTIAENIRYGREVDVMTDEIEKAVKEANAYDFIMKLPQKFTLVGERGAOLSGGQK 540
478 VLPATTIAENIRYGREVDVMTDEIEKAVKEANAYDFIMKLPKFTLVGERGAOLSGGQK 537
541 RIAARALVNPKILLDEATSAALDTESEAVVQVALDKARKGRTTIVIAHRLSTVRNADV 600
538 RIAARALVNPKILLDEATSAALDTESEAVVQVALDKARKGRTTIVIAHRLSTVRNADV 597
601 IAGFDGIVVEKGNHDEMEKGYFKLVMTQTAGNEIELENADESKSIDTLEMSHD 660
598 IAGFDGIVVEKGNHDEMEKGYFKLVMTQTAGNEIELENADESKSIDTLEMSHD 657
661 SSSSLRKRTSRVSQSGQDRKLSYKEALDESIPVSWRIMKMLTWPYFVGVFC 720
658 SSSSLRKRTSRVSQSGQDRKLSYKEALDESIPVSWRIMKMLTWPYFVGVFC 717
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718 AINGGLQPAFAVIFSKIIIGITRNDDAETKQNSNLFSLFLVLGIVSFTTFLQGFTE 777
781 GKAGEILTRELRYMVFMSLRQDVSFDDPKNTTGTALTTRLANDAAQVKAIGSLRAIIT 840
778 GKAGEILTRELRYMVFMSLRQDVSFDDPKNTTGTALTTRLANDAAQVKAIGSLRAIIT 837
841 QNTANLGTGIIISLIYQWQTLTLLAIVPIAIAAGVEMKMSQALDKKELEGAGKIA 900
838 QNTANLGTGIIISLIYQWQTLTLLAIVPIAIAAGVEMKMSQALDKKELEGAGKIA 897
901 TEAIENFRTVSLTQEQKEFHHYDQSLQVPRNSLRKAHIFGITFTSQAMVPSYAGCF 960
898 TEAIENFRTVSLTQEQKEFHHYDQSLQVPRNSLRKAHIFGITFTSQAMVPSYAGCF 957
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958 RFGAYLVHSLMSEFEDVLLVFSVAVFGAMAVQVSSFAPDYAKAKVSAHHIMIEKTPL 1017
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1018 IDSVSTGLKPNLTLEGNVTNEVFNYPTRLDIPVLQSLSEVKKGTALVSGSGGCKS 1077
1081 TVVQLLRFYDPLAGKVLDDGKEIKQLNVQWLRHLGIVSQEPILFDCSIAENIAYGDN 1140
1078 TVVQLLRFYDPLAGKVLDDGKEIKQLNVQWLRHLGIVSQEPILFDCSIAENIAYGDN 1137
1141 RVVSQEBIVRAAEKANTHAFIESLPNKYSTRVGDKGTOLSGGQKORIAARALVRQPHIL 1200
1138 RVVSQEBIVRAAEKANTHAFIESLPNKYSTRVGDKGTOLSGGQKORIAARALVRQPHIL 1197
1201 LLEDEATSAALDESCKVQVQALDKAREGRTICIVIAHRLSTQNADLIVVFQNGRVKRGTH 1260
1198 LLEDEATSAALDESCKVQVQALDKAREGRTICIVIAHRLSTQNADLIVVFQNGRVKRGTH 1257
1261 QOLLAQKGIYFSMVSVQAGAKRQ 1283.
1258 QOLLAQKGIYFSMVSVQAGAKRQ 1280

RESULT 6

Q6PSM2 CANFA
ID Q6PSM2 CANFA PRELIMINARY; PRG; 1281 AA.

AC Q6PSM2; 2004, integrated into UniProtKB/TrEMBL.

DT 05-JUL-2004, sequence version 1.

DE 21-FEB-2006, entry version 13.

DT Multidrug resistance protein 1.

GN Name=MDRI.

OS Canis familiaris (Dog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis
OX NCBI_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Booth-Genthe C.L., Roller C.R., Rushmore T.H.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the ABC transporter family.
CC
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
CC EMBL: AY582533; AA0591647.1; ; mRNA.
DR Ensembl: ENSCARG0000001835; Canis familiaris.
DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0005524; F: ATP binding; IEA.
DR GO: GO:0016887; F: ATPase activity; IEA.
DR GO: GO:0042626; F: ATPase activity, coupled to transmembrane m. .; IEA.
DR GO: GO:0000166; F: nucleotide binding; IEA.
DR GO: GO:0006810; P: transport; IEA.
DR InterPro: IPR003593; AAA_ATPase.
DR InterPro: IPR011527; ABC_TM_1.
DR InterPro: IPR001140; ABC_TM_transp.
DR InterPro: IPR003439; ABC_transp_like.
DR Pfam: PF00664; ABC_membrane_2.
DR Pfam: PF00005; ABC_tran_2.
DR ProDom: PD000006; ABC_transporter; 2.
DR SMART: SM00382; AAA; 2.
DR PROSITE: PS00929; ABC_TM1F; 2.
DR PROSITE: PS02111; ABC_TRANSPORTER_1; 2.
DR PROSITE: PS00893; ABC_TRANSPORTER_2; 2.
DR ATP-binding; Membrane; Nucleotide-binding; Repeat; Transport.
KW
SQ SEQUENCE 1281 AA; 141634 MW; 7832850A11334436 CRC64;

Query Match 91.1%; Score 5869.5; DB 2; Length 1281;
Best Local Similarity 90.5%; Pred. No. 7.9e-292;
Matches 1167; Conservative 56; Mismatches 51; Indels 15; Gaps 5;

QY 1 MDLEGDRNGAEEKNFPLNNKSK-DKKERKKTVSFMSFRYSNWLKLYMVVGTIAAI 59
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QY 60 IHGAGLPLMLVFGDMTDTFANAGNLGDLGALLFNNT-----NSSNITDTPVVA-N-LEED 113
DB 60 IHGAGLPLMLVFGDMTDTFANAGNLGDLGALLFNNT-----ISNKTFFVINESTNTQHNHLEE 112
QY 114 MTRYAYVYSGIGAGVLVAAYIQVSWCLAGROIHRIKROFFHAIMRQEIFGWFDVHDVE 173
DB 113 MTRYAYVYSGIGAGVLVAAYIQVSWCLAGROIHRIKROFFHAIMRQEIFGWFDVHDVE 172
QY 174 LNTRLTDDSVKINEGIDKLGIMFQSMATPFTGTFVIGFTGWLTLVLAISVPLGSLAA 233
DB 173 LNTRLTDDSVKINEGIDKLGIMFQSMATPFTGTFVIGFTGWLTLVLAISVPLGSLAA 232
QY 234 VWAKILSSFTDKELLAYAKAGAAVEVLAARTVIAFGGOKELERYKNLEAKRIGIK 293
DB 233 IWAKILSSFTDKELLAYAKAGAAVEVLAARTVIAFGGOKELERYKNLEAKRIGIK 292
QY 294 KAITANISIGAAFLLIYASALAFWYGTTLVLKEYSISGOVLTVFFSVLIGAFSVGOASP 353
DB 293 KAITANISIGAAFLLIYASALAFWYGTTLVLKEYSISGOVLTVFFSVLIGAFSVGOASP 352
QY 354 SIEAFANARGAAPEIFKIDNKPISIDYSKSGHKPDNKGKLNLEFRNVHFSYPSRKEVKIL 413
DB 353 SIEAFANARGAAPEIFKIDNKPISIDYSKSGHKPDNKGKLNLEFRNVHFSYPSRKEVKIL 412
QY 414 KGLNLVQSGQTVALVNSCGSKSTTQVMQRLYDPTGEMVSDGQDRTINVEFLREII 473
DB 413 KGLNLVQSGQTVALVNSCGSKSTTQVMQRLYDPTGEMVSDGQDRTINVEFLREII 472
QY 474 GVVSQBPVLPATTIAENIRYGREVDVMTDEIEKAVKEANAYDFIMKLPQKFTLVGERGAQ 533

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DB 1 MDLEGRNGGAEKKNFFKLNKSKKDKKPKPTVSFVSFMYRYSNWLDKLYMVVGTAAII 60
QY 61 HGAGLPLMLVFGDMTDTFANAGNLGDLGALLFNNTSSNITDTVPVWNLLEEDMTRYAY 120
DB 61 HGAGLPLMLVFGDMTDTFANAGNLGDLGALLFNNTSSNITDTVPVWNLLEEDMTRYAY 117
QY 121 YSGGAGVLVAAYIQVSFWCLAAAGQIHKIRKQFFHAIMROEIGFVDHVDGELNTRLTD 180
DB 118 YSGGAGVLVAAYIQVSFWCLAAAGQIHKIRKQFFHAIMROEIGFVDHVDGELNTRLTD 177
QY 161 DVSKINEGIDGKIGMFFQSMATFFTGPIVGFTRGWKLTIVILAI SPVLGLSAVWAKILS 240
DB 178 DVSKINEGIDGKIGMFFQSMATFFTGPIVGFTRGWKLTIVILAI SPVLGLSAVWAKILS 237
QY 241 SFTDKELLAYAKAGAVAEVLAAIRTVIAGFGQKKELERYNKNLEAKRIGIKKAITANI 300
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QY 301 SIGAFLIYASYALAFWYGTITLVLSKEYSIGOVLTVPFVSLIGAFSGQASPSIEAFAN 360
DB 298 SIGAFLIYASYALAFWYGTITLVLSKEYSIGOVLTVPFVSLIGAFSGQASPSIEAFAN 357
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DB 358 ARGAAFEI PKIDNKPSIDSYSGHKKPDNIKGNLEFRNVHFSYPSRKEVKILKGLNLKV 417
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DB 418 QSGQTVLVGNSGCGKSTTVLMQRLYDPTGEMVSDGQDINTINVRFLREIIGVVSQBP 477
QY 481 VLFATTAENIRYGRDVTMDIEKAVKEANAYDTIMKLPQKFDTLVGERGAQLSGGQK 540
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DB 598 IAGFDGVIVKGNHDELMEKGIYFKLVMTQAGNEIELENADESKSEIDTLESSH 657
QY 661 SGSSILIRKSTRSRRSGGQDKLSTKEALDESIPPVSWFMKMLNLTWPFVVGVC 720
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QY 721 AIINGLOPAPAVIFSKIIIGIFTRNDDAETKQNSNLFSLFLVLGIVSFIFFLQGF 780
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DB 838 QNIANLGTIISLISYGLQTLTLLAIIPVIAIAGVVENKMLSGQALDKKLEGAAGKTA 897
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DB 1018 IDSYSTEGIKPNTLGNVTNFWNFYPTRLDIPVLOGLSLEVKGTALVGSQCGK 1077
QY 1081 TVVQLLRFYDPLAGKVLLDGKEIKQLNVQWLAHGLIVSOBPIIFDCSISENIAYGNS 1140

DB 1078 TVVQLLRFYDPLAGKVLLDGKEIKQLNVQWLAHGLIVSOBPIIFDCSISENIAYGNS 1137
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DB 1138 RVVQEEITVRAAKANIHAFIESLPNKYSTRVGDKGTQLSGGQKORIAARALVRQPHIL 1197
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QY 1261 QOLLAQGIYFSMVSVQAGAKRQ 1283
DB 1258 QOLLAQGIYFSMVSVQAGAKRQ 1280
RESULT 6
US-09-584-586-2
Sequence 2, Application US/09584586
Patent No. 6933150
GENERAL INFORMATION:
APPLICANT: Sorrentino, Brian
APPLICANT: Bunting, Kevin
TITLE OF INVENTION: EXPANSION OF HEMATOPOIETIC STEM CELLS TRANSDUCED WITH
FILE OF INVENTION: MDR-1 METHODS OF USE THEREOF
FILE REFERENCE: 1340-1-021CIP
CURRENT APPLICATION NUMBER: US/09/584,586
CURRENT FILING DATE: 2000-05-31
EARLIER APPLICATION NUMBER: US 60/086,988
EARLIER FILING DATE: 1998-05-28
EARLIER APPLICATION NUMBER: PCT/US99/11825
EARLIER FILING DATE: 1999-05-27
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 2
LENGTH: 1280
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Human MDR 185-G
US-09-584-586-2
Query Match 96.4%; Score 6212.5; DB 2; Length 1280;
Best Local Similarity 96.5%; Pred. No. 0;
Matches 1238; Conservative 18; Mismatches 24; Indels 3; Gaps 1;
QY 1 MDLEGRNGGAEKKNFFKLNKSKKDKKPKPTVSFVSFMYRYSNWLDKLYMVVGTAAII 60
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DB 61 HGAGLPLMLVFGDMTDTFANAGNLGDLGALLFNNTSSNITDTVPVWNLLEEDMTRYAY 117
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1078 TVVOLLERFYDPLAGKVLDDGKEIKOLNVQWLAHGLGIVSQBPILFDCSISENIAVDNS 1137
1141 RVVSQBEIVRAAEKANTHAFIESIPNKYSTVGVKGTQSLSGGOKORIAIARALVRPHIL 1200
1138 RVVSQBEIVRAAEKANTHAFIESIPNKYSTVGVKGTQSLSGGOKORIAIARALVRPHIL 1197
1201 LLDDEATSEKVVQVQALDKARKGRTTIVIAHRLSTIONADLIIVFQNGRVKXHGTH 1260
1198 LLDDEATSEKVVQVQALDKARKGRTTIVIAHRLSTIONADLIIVFQNGRVKXHGTH 1257
1261 QQLLAQKGIYFSMVSVQAGTKRQ 1283
1258 QQLLAQKGIYFSMVSVQAGTKRQ 1280

RESULT 7
US-09-767-594-2
Sequence 2, Application US/09767594
Patent No. 6521635
GENERAL INFORMATION:
APPLICANT: Bates, Susan
APPLICANT: Robey, Robert
APPLICANT: The Government of the United States of America
APPLICANT: As represented by the Secretary of the
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Inhibition of MXR Transport by Acridine Derivatives

FILE REFERENCE: 015280-402100US
CURRENT APPLICATION NUMBER: US/09/767,594
CURRENT FILING DATE: 2001-01-22
PRIOR APPLICATION NUMBER: US 60/177,410
PRIOR FILING DATE: 2000-01-20
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 1280
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: human P-glycoprotein (Pgp)/multi-drug resistance 1
OTHER INFORMATION: (Mdr-1) ATP-binding cassette (ABC transporter)
OTHER INFORMATION: protein
US-09-767-594-2
Query Match 96.3%; Score 6203.5; DB 2; Length 1280;
Best Local Similarity 96.4%; Pred. No. 0;
Matches 1237; Conservative 18; Mismatches 25; Indels 3; Gaps 1;
QY 1 MDLEGRNGGAEKKNFFKLNKSKDKKERKPTVSVFSMFYSNWLKLYMVVGTLLAII 60
DB 1 MDLEGRNGGAEKKNFFKLNKSKDKKERKPTVSVFSMFYSNWLKLYMVVGTLLAII 60
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DB 61 HGAGLPLMLVFGDMTDTFANAGMLGDLGALLFNTNTHSSNITDTPVNNLEEDMTRYAY 117
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QY 241 SPTDKELLAYAKAGAVAEVLAARTVIAFGOKKELERYNNKLEAKRIGIKKAITANI 300
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QY 301 SIGAFLIYIYALAFWYGTTLVLSKEYSGQVLTFFSVLIGAFSQAQSPSIEAFAN 360
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QY 361 ARGAAFEIPKIIDNKPSIDSYSGKHPDNKGNLEFRNVHFSYPSRKEVKILKGLNLKV 420
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QY 421 QSGQTVLVGNSGCGKSTTVQMLQRLYDPTGKWSVDGQDRTINVRFLREIIGVVSQBP 480
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QY 481 VLPATTIAENIRYGRDVTMDIEKAVKEANAYDFIMKLPQKFDTLVGERGQALSGGQK 540
DB 478 VLPATTIAENIRYGRDVTMDIEKAVKEANAYDFIMKLPQKFDTLVGERGQALSGGQK 537
QY 541 RIAIARALVRNPKILLDEATSEAVQVQALDKARKGRTTIVIAHRLSTVRNADV 600
DB 538 RIAIARALVRNPKILLDEATSEAVQVQALDKARKGRTTIVIAHRLSTVRNADV 597
QY 601 IAGFDGVIYKGNHDELMEKGIYFKLVTMOTAGNEIELENADESKSEIDTLESSH 660
DB 598 IAGFDGVIYKGNHDELMEKGIYFKLVTMOTAGNEIELENADESKSEIDTLESSH 657
QY 661 SGSSLRKSTRSRVRSVRSQDQKSTKEALDESIPPVSWFRIMKLNLTWPFVVGVC 720
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QY 721 AIINGLOPAPAVIFSKIIIGIFTRNDDEATKQNSNLFSLFLVLGIVSFIITFFLOGTF 780
DB 718 AIINGLOPAPAVIFSKIIIGIFTRNDDEATKQNSNLFSLFLVLGIVSFIITFFLOGTF 777

Query Match		96.3%;	Score 6203.5;	DB 2;	Length 1280;	
Best Local Similarity		96.4%;	Pred. No. 0;			
Matches 1237;		Conservative 18;	Mismatches 25;	Indels 3;	Gaps 1;	
QY	1	MDLEGDRNGAEGKKNPFKLNKSKKKKPKPTVSFVSFMYRNWLDKLYMVVGTAAII	60			
DB	1	MDLEGDRNGAEGKKNPFKLNKSKKKKPKPTVSFVSFMYRNWLDKLYMVVGTAAII	60			
QY	61	HGAGLPLMLVFGDMTDTFANAGNLGDLGALLFNNTSSNITDTVPVNNLEEDMTYAY	120			
DB	61	HGAGLPLMLVFGDMTDTFANAGNLGDLGALLFNNTSSNITDTVPVNNLEEDMTYAY	117			
QY	121	YSIGIGAGLVAAIYQVSWFCLAAAGRQIHKIRKQFHAIHQEIGWFDVHVGELNRLTD	180			
DB	118	YSIGIGAGLVAAIYQVSWFCLAAAGRQIHKIRKQFHAIHQEIGWFDVHVGELNRLTD	177			
QY	181	DVSKINEGIGDKIGMPFQSMATPTFTGIVGTGKTLVLAIQVGLSAVAKILS	240			
DB	178	DVSKINEGIGDKIGMPFQSMATPTFTGIVGTGKTLVLAIQVGLSAVAKILS	237			
QY	241	SFTDKELLAYAKAGAAVEVLAAIRTVIAFGGKCELEKRYNKNLEENRIGIKAITANI	300			
DB	238	SFTDKELLAYAKAGAAVEVLAAIRTVIAFGGKCELEKRYNKNLEENRIGIKAITANI	297			
QY	301	SIGAAFLLIYASALAFWYGTTLVLSEYISIGQVLTVPFVSIGASVGSPIEFAN	360			
DB	1021	IDSYSTEGKLPNTLEGNVTFFVFNPTTRDIPVLQGLSLEVKGQTLALVSSGCGKS	1080			
Query Match						
Best Local Similarity		96.3%;	Score 6203.5;	DB 2;	Length 1280;	
Matches 1237;		Conservative 18;	Mismatches 25;	Indels 3;	Gaps 1;	
QY	1	MDLEGDRNGAEGKKNPFKLNKSKKKKPKPTVSFVSFMYRNWLDKLYMVVGTAAII	60			
DB	1	MDLEGDRNGAEGKKNPFKLNKSKKKKPKPTVSFVSFMYRNWLDKLYMVVGTAAII	60			
QY	61	HGAGLPLMLVFGDMTDTFANAGNLGDLGALLFNNTSSNITDTVPVNNLEEDMTYAY	120			
DB	61	HGAGLPLMLVFGDMTDTFANAGNLGDLGALLFNNTSSNITDTVPVNNLEEDMTYAY	117			
QY	121	YSIGIGAGLVAAIYQVSWFCLAAAGRQIHKIRKQFHAIHQEIGWFDVHVGELNRLTD	180			
DB	118	YSIGIGAGLVAAIYQVSWFCLAAAGRQIHKIRKQFHAIHQEIGWFDVHVGELNRLTD	177			
QY	181	DVSKINEGIGDKIGMPFQSMATPTFTGIVGTGKTLVLAIQVGLSAVAKILS	240			
DB	178	DVSKINEGIGDKIGMPFQSMATPTFTGIVGTGKTLVLAIQVGLSAVAKILS	237			
QY	241	SFTDKELLAYAKAGAAVEVLAAIRTVIAFGGKCELEKRYNKNLEENRIGIKAITANI	300			
DB	238	SFTDKELLAYAKAGAAVEVLAAIRTVIAFGGKCELEKRYNKNLEENRIGIKAITANI	297			
QY	301	SIGAAFLLIYASALAFWYGTTLVLSEYISIGQVLTVPFVSIGASVGSPIEFAN	360			
DB	1021	IDSYSTEGKLPNTLEGNVTFFVFNPTTRDIPVLQGLSLEVKGQTLALVSSGCGKS	1080			

RESULT 11
US-09-817-762-3
Sequence 3, Application US/09817762
Patent No. 6858774

GENERAL INFORMATION
APPLICANT: Spalding, Edgar P.
APPLICANT: No. 6858774, Bosh
TITLE OF INVENTION: MDR-Like ABC Transporter Gene From
TITLE OF INVENTION: Plants
FILE REFERENCE: 13238-00061
CURRENT APPLICATION NUMBER: US/09/817,762
CURRENT FILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: PCT/US99/22363
PRIOR FILING DATE: 1999-09-24
PRIOR APPLICATION NUMBER: US 60/101,814
PRIOR FILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 1280
TYPE: PRT
ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
PUBLICATION ACCESSION NUMBER: Genbank P08183
DATABASE ENTRY DATE: 1997-11-01
US-09-817-762-3

Query Match		96.3%;	Score 6203.5;	DB 2;	Length 1280;
Best Local Similarity		96.4%;	Pred. No. 0;		
Matches 1237;		Conservative 18;	Mismatches 25;	Indels 3;	Gaps 1;
QY	1	MDLEGDRNGAEGKKNPFKLNKSKKKKPKPTVSFVSFMYRNWLDKLYMVVGTAAII	60		
DB	1	MDLEGDRNGAEGKKNPFKLNKSKKKKPKPTVSFVSFMYRNWLDKLYMVVGTAAII	60		
QY	61	HGAGLPLMLVFGDMTDTFANAGNLGDLGALLFNNTSSNITDTVPVNNLEEDMTYAY	120		
DB	61	HGAGLPLMLVFGDMTDTFANAGNLGDLGALLFNNTSSNITDTVPVNNLEEDMTYAY	117		
QY	121	YSIGIGAGLVAAIYQVSWFCLAAAGRQIHKIRKQFHAIHQEIGWFDVHVGELNRLTD	180		
DB	118	YSIGIGAGLVAAIYQVSWFCLAAAGRQIHKIRKQFHAIHQEIGWFDVHVGELNRLTD	177		
QY	181	DVSKINEGIGDKIGMPFQSMATPTFTGIVGTGKTLVLAIQVGLSAVAKILS	240		
DB	178	DVSKINEGIGDKIGMPFQSMATPTFTGIVGTGKTLVLAIQVGLSAVAKILS	237		
QY	241	SFTDKELLAYAKAGAAVEVLAAIRTVIAFGGKCELEKRYNKNLEENRIGIKAITANI	300		
DB	238	SFTDKELLAYAKAGAAVEVLAAIRTVIAFGGKCELEKRYNKNLEENRIGIKAITANI	297		
QY	301	SIGAAFLLIYASALAFWYGTTLVLSEYISIGQVLTVPFVSIGASVGSPIEFAN	360		

298 SIGAAFLIIYASALAFWYGTTLVLSGEYSIGQVLTVPFVSLVIGAFVSGQASPSIEAFAN 357
361 ARGAAFEIPIKIIDNKPSIDTSKSGHKPDNKNLEPRNVHPSPSRKEVKILKGLNLKV 420
358 ARGAAFEIPIKIIDNKPSIDTSKSGHKPDNKNLEPRNVHPSPSRKEVKILKGLNLKV 417
421 QSGQTVLAVGNSGCGKSTTVOLMORLYDPTGEMVSDGQDRTINVRFLREIIGVVSQEP 480
418 QSGQTVLAVGNSGCGKSTTVOLMORLYDPTGEMVSDGQDRTINVRFLREIIGVVSQEP 477
481 VLPATTIAENIRYGRBVTWDEIEKAVKEANAYDFIMKLPKQFDTLVGERGAQLSGGQK 540
478 VLPATTIAENIRYGRBVTWDEIEKAVKEANAYDFIMKLPKQFDTLVGERGAQLSGGQK 537
541 RIAIARALVRNPKILLDEATSALDTESEAVVQVVALDKARKGRTTIVIAHRLSTVRNADV 600
538 RIAIARALVRNPKILLDEATSALDTESEAVVQVVALDKARKGRTTIVIAHRLSTVRNADV 597
601 IAGFDGVIYVKGNDHDELMKSGIYFKLVMTQTAGNEIELENADESKSEIDTLEMSSHD 660
598 IAGFDGVIYVKGNDHDELMKSGIYFKLVMTQTAGNEIELENADESKSEIDALEMSSND 657
661 SGSSLIKRSTRSRVRSQODRKLSTKEALDESIPVPSFWIRIMKLNLTWPYFVVGVC 720
658 SRSSLIKRSTRSRVRSQODRKLSTKEALDESIPVPSFWIRIMKLNLTWPYFVVGVC 717
721 AINGGLQPAFAVIFSKIIIGITFRNDDAETKRONSLFSLFLVIGIVSFITFLOQFTF 780
718 AINGGLQPAFAVIFSKIIIGITFRNDDAETKRONSLFSLFLVIGIVSFITFLOQFTF 777
781 KGAELTKRLRYMVFRSMLQDVSFDDPKNTTGALTTRLANDAAQVKGAGISRLAIT 840
778 KGAELTKRLRYMVFRSMLQDVSFDDPKNTTGALTTRLANDAAQVKGAGISRLAIT 837
841 QNIANLGTGIIISLYGQHLTLLIAIYPIITAGVEMKMLSGQALKDKELEGAGKIA 900
838 QNIANLGTGIIISLYGQHLTLLIAIYPIITAGVEMKMLSGQALKDKELEGAGKIA 897
901 TEAIENFRTVSLTQEQKFEHMYDOSLQVPRYNSLRKAHIFGITPSTQAMWYFSGCF 960
898 TEAIENFRTVSLTQEQKFEHMYDOSLQVPRYNSLRKAHIFGITPSTQAMWYFSGCF 957
961 RFGAYLVAHLSMEDVLLVFSVAVFGAMAVQVSSFPADYAKAKISAAHIIIMIEKTPL 1020
958 RFGAYLVAHLSMEDVLLVFSVAVFGAMAVQVSSFPADYAKAKISAAHIIIMIEKTPL 1017
1021 IDSYSTEGKLENTLEGNTFNEVFNYPTRLDIPVLQGLSLEVKKGOTLALVSGSGGKS 1080
1018 IDSYSTEGKLENTLEGNTFNEVFNYPTRLDIPVLQGLSLEVKKGOTLALVSGSGGKS 1077
1081 TVVOLLERFYDPLAGKVLDDKEIKOLNVQMLRAHIGIVSOEPILFDCSISENTAYGDSN 1140
1078 TVVOLLERFYDPLAGKVLDDKEIKOLNVQMLRAHIGIVSOEPILFDCSISENTAYGDSN 1137
1141 RVVSOEELVRAAKENIHAFTESLPNKYSTYRVDKGTOLSGQOKORIAIARALVRQPHIL 1200
1138 RVVSOEELVRAAKENIHAFTESLPNKYSTYRVDKGTOLSGQOKORIAIARALVRQPHIL 1197
1201 LLDATSALDTESEKVVQEALDKAREGRTTIVIAHRLSTIONADLIIVFQNGRVEKGHTH 1260
1198 LLDATSALDTESEKVVQEALDKAREGRTTIVIAHRLSTIONADLIIVFQNGRVEKGHTH 1257
1261 QOLLAQKGIYFSMVSVOAGKRO 1283
1258 QOLLAQKGIYFSMVSVOAGKTRQ 1280

RESULT 12

US-09-584-586-4
Sequence 4, Application US/09584586
Patent No. 6933150
Additional INFORMATION:
Inventor: Sorrentino, Brian

APPLICANT: Bunting, Kevin
TITLE OF INVENTION: EXPANSION OF HEMATOPOIETIC STEM CELLS TRANSDUCED WITH
FILE OF INVENTION: MDR-1 METHODS OF USE THEREOF
FILE REFERENCE: 1340-1-021CIP
CURRENT APPLICATION NUMBER: US/09/584,586
CURRENT FILING DATE: 2000-05-31
EARLIER APPLICATION NUMBER: US 60/086,988
EARLIER FILING DATE: 1998-05-28
EARLIER APPLICATION NUMBER: PCT/US99/11825
EARLIER FILING DATE: 1999-05-27
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 1280
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Human MDR 185-V
US-09-584-586-4

Query Match 96.3%; Score 6203.5; DB 2; Length 1280;
Best Local Similarity 96.4%; Pred. No. 0;
Matches 1237; Conservative 18; Mismatches 25; Indels 3; Gaps 1;
Qy 1 MDLEGDRNGAEGKKNPFKLNKSKDKKPKPTVSFMSFRYSNMWLDKLYMVVGTAAII 60
Db 1 MDLEGDRNGAEGKKNPFKLNKSKDKKPKPTVSFMSFRYSNMWLDKLYMVVGTAAII 60
Qy 61 HGAGLPLMLVFGDMTDTFANAGNLGDLGALLFNNTNSSNITDTVPVMLLEDMTRYAY 120
Db 61 HGAGLPLMLVFGDMTDTFANAGNLGDLGALLFNNTNSSNITDTVPVMLLEDMTRYAY 117
Qy 121 YSGIGAGLVAAIYQVSPWCLAAGROIHKIRQFHAIMRQEIIGMDFDHDVDELNRLTD 180
Db 118 YSGIGAGLVAAIYQVSPWCLAAGROIHKIRQFHAIMRQEIIGMDFDHDVDELNRLTD 177
Qy 181 DVSKINEGIGDKIMGFQSQMATPFTGFIYVGRGWLTLVILAIISVLSAAVAKILS 240
Db 178 DVSKINEGIGDKIMGFQSQMATPFTGFIYVGRGWLTLVILAIISVLSAAVAKILS 237
Qy 241 SFTDKELLAYAKAGAVAEVLAIRTVIAFGQKKELERYKNLEAKRIGIKKAITANI 300
Db 238 SFTDKELLAYAKAGAVAEVLAIRTVIAFGQKKELERYKNLEAKRIGIKKAITANI 297
Qy 301 SIGAAFLIIYASALAFWYGTTLVLSGEYSIGQVLTVPFVSLVIGAFVSGQASPSIEAFAN 360
Db 298 SIGAAFLIIYASALAFWYGTTLVLSGEYSIGQVLTVPFVSLVIGAFVSGQASPSIEAFAN 357
Qy 361 ARGAAFEIPIKIIDNKPSIDTSKSGHKPDNKNLEPRNVHPSPSRKEVKILKGLNLKV 420
Db 358 ARGAAFEIPIKIIDNKPSIDTSKSGHKPDNKNLEPRNVHPSPSRKEVKILKGLNLKV 417
Qy 421 QSGQTVLAVGNSGCGKSTTVOLMORLYDPTGEMVSDGQDRTINVRFLREIIGVVSQEP 480
Db 418 QSGQTVLAVGNSGCGKSTTVOLMORLYDPTGEMVSDGQDRTINVRFLREIIGVVSQEP 477
Qy 481 VLPATTIAENIRYGRBVTWDEIEKAVKEANAYDFIMKLPKQFDTLVGERGAQLSGGQK 540
Db 478 VLPATTIAENIRYGRBVTWDEIEKAVKEANAYDFIMKLPKQFDTLVGERGAQLSGGQK 537
Qy 541 RIAIARALVRNPKILLDEATSALDTESEAVVQVVALDKARKGRTTIVIAHRLSTVRNADV 600
Db 538 RIAIARALVRNPKILLDEATSALDTESEAVVQVVALDKARKGRTTIVIAHRLSTVRNADV 597
Qy 601 IAGFDGVIYVKGNDHDELMKSGIYFKLVMTQTAGNEIELENADESKSEIDTLEMSSHD 660
Db 598 IAGFDGVIYVKGNDHDELMKSGIYFKLVMTQTAGNEIELENADESKSEIDALEMSSND 657
Qy 661 SGSSLIKRSTRSRVRSQODRKLSTKEALDESIPVPSFWIRIMKLNLTWPYFVVGVC 720
Db 658 SRSSLIKRSTRSRVRSQODRKLSTKEALDESIPVPSFWIRIMKLNLTWPYFVVGVC 717
Qy 721 AINGGLQPAFAVIFSKIIIGITFRNDDAETKRONSLFSLFLVIGIVSFITFLOQFTF 780